

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number:

TO: Minh-Tam Davis

Location: rem/3A24/3C18

Art Unit: 1642

Friday, June 09, 2006

Case Serial Number: 09/743825

From: Mary Jane Ruhl

**Location: Biotech-Chem Library** 

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

#### Search Notes

Examiner Davis,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



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# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number

TO: Minh-Tam Davis

Location: rem/3A24/3C18

Art Unit: 1642

**Thursday, May 04, 2006** 

Case Serial Number: 09/743825

From: Noble Jarrell

**Location: Biotech-Chem Library** 

**Rem 1B71** 

Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes			
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#### November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases: older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

.rapbm (Published\_Applications\_AA\_New).

THE TOP BONK USC.

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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7.3.6.28

#### STIC-Biotech/ChemLib

187401

ME

From:

Chan, Christina

Sent:

Thursday, April 27, 2006 10:52 AM

To:

Davis, Minh-Tam; STIC-Biotech/ChemLib

Subject:

RE: Rush search request for 09/743825

#### Please with Thanks Chris

#### Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From:

Davis, Minh-Tam

Sent:

Thursday, April 27, 2006 10:15 AM

To:

Chan, Christina

Subject:

Rush search request for 09/743825

Please search for interference only:

1) SEQ ID NO:1.

2) Nucleotides 77-1753 of SEQ ID NO:1.

3) SEQ ID NO: 7, 8 and 10, with size limitation for the data in the database to the size of the corresponding sequences.

THANK YOU

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

A 4	
Searcher: Iwle	
Searcher Phone:	
Date Searcher Picked up:	
Date completed: 515(0	b
Searcher Prep Time: 5	
Online Time:	

Ţy	pe of Search
NA# <u>Υ</u>	
S/L:	_ Oligomer:
Encode/T	ransl:
Structure	#:Text:
Inventor:	Litigation:

**********	
Vendors and cost where applicable	
STN:	
DIALOG:	
QUESTEL/ORBIT:	
LEXIS/NEXIS:	
SEQUENCE SYSTEM: Campuge	ı
W/W/W/Internet	

Other (Specify):\_\_

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73622

#### **STIC-Biotech/ChemLib**

192 242

MG

From:

Chan, Christina

Sent:

Wednesday, June 07, 2006 1:36 PM

To: Subject: Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/743825

#### Please aush! Thanks Chris

#### Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Wednesday, June 07, 2006 1:32 PM

To:

Chan, Christina

Subject:

Rush search request for 09/743825

Please search in commercial database, issued patent files and PGPUB:

SEQ ID NO:7, 8, 10 with size limitation for the sequences in the database to the size of the corresponding sequences. Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

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Type of Search

NA#\_\_\_\_\_\_ AA#:\_\_\_\_\_

S/L:\_\_\_\_\_ Oligomer:\_\_\_\_\_

Encode/Transl:\_\_\_\_\_

Structure #:\_\_\_\_\_ Text:\_\_\_

Inventor: Litigation:

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

Ihis rage blank (uspto)

Fri Jun

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

June Run on:

9, 2006, 00:36:21; Search time 289 Seconds (without alignments) 482.509 Million cell updates/sec

Title: Perfect score:

US-09-743-825-10 20 1 gaccgcatagacttctcaga 20 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

5244920 seqs, 3486124231 residues Searched:

Total number of hits satisfying chosen parameters:

2681012

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2001as:\*
geneseqn2001bs:\*
geneseqn2002bs:\*
geneseqn2003as:\*
geneseqn2003as:\*
geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2005s:\* geneseqn1990s:\*geneseqn2000s:\* geneseqn1980s:\* N\_Geneseq\_8:\* :01 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2006s:\*

	Description	Asys May 50446 Unimen DD2	Askga486 DCP prime	Aad62200 Human hae	Aee31152 Haemophil	Adt00440 Novel mut	Adw95798 Human TFR	Adz44776 Human tra	Aca08287 Necrosis	Aca06680 NFKB sub-	Aaz48549 Human TNF	Abt05045 TNFR1 exp	Adro6077 Human TNF	Adg73193 Pseudomon	Adl12249 Pseudomon	Adi79866 Mouse HMG	Adi79673 Mouse HMG	Adw95797 Human TFR	Adx57319 Forward P
SUMMARIES	ΙD	AA250446	AAX93486	) AAD62200	5 AEE31152	1 ADT00440	I ADW95798	I ADZ44776	ACA08287	ACA06680	AAZ48549	ABT05045	1 ADR06077	) ADG73193	) ADL12249	: ADI79866	: ADI79673	L ADW95797	4 ADX57319
	* Duery Match Length DB	20.3	200	20 10	19 15	20 13	20 14	20 14	17 8	17 8	18 3	18 6	18 13	19 10	19 10	20 12	20 12	20 14	20 14
	Query Match I	0001	0.69	0.99	63.0	63.0	63.0	63.0	62.0	62.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0
	Score	20	13.8	13.2	12.6	12.6	12.6	12.6	12.4	12.4	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2
	Result No.	-	10	o O	Ω 4	2	9	7	80	σ	c 10	c 11	c 12	13	14	15	c 16	17	18

Adz44775 Human tra	Aag32840 Microsate	Aag57863 Primer pa		Aac60963 TATA box-	Adb42063 Tumour su	Adi48431 Human tum	Aag94315 Human cyt	Aav30475 Canine be	Aec47173 Antisense	Aec47021 Antisense	Aec47477 Antisense	Aec47325 Antisense	Aebs0764 Human ADA	Aeb50960 Human ADA	Aee22319 Liver fib	Aav33985 Primer CT	Aaz24116 Primer CT	Abz91284 Human oli	Abd27514 AA486238-	Aad11750 Human AAG	Adw79353 Human ace	Adw78939 Human ace	Aeall754 Human ACA	Aeal1340 Human ACA	Abk41518 Human CTN	Abs59713 Human dam	
ADZ44775	AAQ32840	AAQ57863	AAZ21763	AAC60963	ADB42063	ADI48431	AAQ94315	AAV30475	AEC47173	AEC47021	AEC47477	AEC47325	AEB50764	AEB50960	AEE22319	AAV33985	AAZ24116	ABZ91284	ABD27514	AAD11750	ADW79353	ADW78939	AEA11754	AEA11340	ABK41518	ABS59713	
14	0	20																									
20	20	20	70	70	17	17	18	18	18	18	18	18	19	19	19	50	50	20	20	13	19	19	19	19	50	20	
61.0	0.09	0.09	0.09	60.09	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	
12.2	12	12	12	12	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.6	11.6	11.6	11.6	•	•	11.6	
19	20	21	22	23	24	c 25	c 26	27	c 28	c 29	c 30	c 31	c 32	33	34	35	36	c 37	c 38	39	40	c 41	42	c 43	44	45	

## ALIGNMENTS

PB39; human; prostate cancer; PC; chromosome llpll.1-11.2; cancer; prostate epithelium; splicing mechanism; early diagnosis; progression; precancerous cell; metastatic potential; non-neoplastic prostate disease; expressed sequence tag; EST; PCR primer; ss. Human PB39 specific 3' RACE primer. AAZ50446 standard; DNA; 20 BP. 99WO-US016831. 18-MAY-2000 (first entry) WO200005376-A1. Homo sapiens. 23-JUL-1999; 03-FEB-2000. AAZ50446; AAZ50446 

98US-0094137P 24-JUL-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES. Liotta LA; Chuaqui RF, Cole KA,

WPI; 2000-182700/16.

Novel gene which is dysregulated in prostate cancer useful for diagnosing cancer.

Claim 5; Page 18; 51pp; English.

The present sequence is the human PB39 3' specific RACE primer, from EST clone AAR00504. It is used to determine the complete nucleotide sequence of PB39 cDNA, isolated from human pancresa cDNA library using RACE. The PB39 gene that is dysregulated in prostate cancer has homology to the EST AAR00504. PB39 gene is located on chromosome lipil.1-11.2. Abnormally

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high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of precancerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX94884- AAX95879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                  Score 20; DB 3; Length 20; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                     0; Indels
                                                                                                                           differing aggressiveness and metastatic potential
                                                                                                                                                              Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 1595; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                         GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                     1 GACCGCATAGACTTCTCAGA
                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97FR-00014673,
98US-0107078P,
                                                                                                                                                                                                                                                                                                                                                                                           AAX93486 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydophila pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
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04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                AAX93486;
                                                                                                                                                                                                                                                                                                                                                             RESULT 2
                                                                                                                                                                                                                                                                                                                                                                             AAX93486
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The invention relates to a compound targetted to a nucleic acid molecule encoding haematopoietic cell protein tyrosine kinase. The compound inhibits the expression of haematopoietic cell protein tyrosine kinase and it specifically hybridises with the nucleic acid molecule encoding the tyrosine kinase or with at least an 8-nucleobase portion of an active site on the nucleic acid molecule encoding the tyrosine kinase. The antisense compounds are useful for modulating the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematopoietic cell protein tyrosine kinase and treating diseases or conditions associated with the expression of the tyrosine kinase, such as hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a viral infection. The antisense compounds are also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in
                                                                                                                                                                                                                                                 Haematopoietic cell; tyrosine kinase; hyperproliferative disorder; cancer; therapy; inflammation; diabetes; viral infection; inflammation; tumour; cytostatic; virucide; antisense therapy; antisense; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorothioate backbone; All cytidines are 5-methyl cytidines"
                                                                                                                                                                                                                  Human haematopoietic cell tyrosine kinase antisense oligo ISIS #150755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides targeted to nucleic acids encoding hematopoietic cell protein tyrosine kinase, useful for diagnosing treating cancer (e.g. leukemia), inflammation, diabetes or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "2'-0-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; Page 26; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                     phosphorothioate backbone; ss.
                      3 GACCGCATAAACTTATC 19
 GACCGCATAGACTTCTC 17
                                                                                                                AAD62200 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2001; 2001US-00007010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2001; 2001US-00007010.
                                                                                                                                                                                  15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borchers AH, Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-811000/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003125275-A1
                                                                                                                                                                                                                                                                                                                                                                                                   modified base
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                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                   AAD62200;
н
                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                 AAD62200/
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Gaps

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69.0%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 2.7e+03; ive 0; Mismatches 2; Indels

15; Conservative

Best\_Local\_Similarity Matches 15; Conserv

Query Match

(4) making (M2) ar altering a coding

AEE31211, AEE31241, AEE31246, AEE31263 and AEE31231;

H. influenzae with reduced virulence, which involves altering a coding sequence in an H. influenzae to comprise a mutation, the non-mutagenized coding sequence comprising a nucleotide sequence chosen from AREN1062, AREN1130, AREN1140, AREN1155, AREN12111, AREN1241, AREN1241, AREN1241, AREN1241, AREN1241, AREN1253, and AREN1211, and determining if the H. influenzae comprising the mutation has reduced virulence compared to an H. influenzae that does not comprise the mutation; (5) an H. influenzae obtained by (M2); and (6) a vaccine composition comprising the H. influenzae. (I) is useful for reducing the virulence of H. influenzae to be used as a vaccine composition, and for decreasing the growth rate of a microorganism. The present sequence represents a PCR primer for a H. influenzae trxB coding sequence is used in the exemplification of the present invention.

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The invention relates to an isolated polypeptide (I) critical for the survival of Haemophilus sp. comprising an amino acid sequence having at least 95% structural similarity with an amino acid sequence chosen from AEE31317, AEE313132, AEE31345, AEE31353, AEE31354 and AEE31317, AEE313130, AEE31345, AEE31345, AEE31354 and AEE31358. Also described: (I) an isolated polynucleotide (II) critical for the aurvival of Haemophilus sp. comprising a nucleotide sequence having at least 95% structural similarity with nucleotide sequence chosen from a coding sequence in AEE31062, AEE31130, AEE31140, AEE31155, AEE31156, CC AEE31211, AEE31241, AEE31246, and AEE31231, and its complements, and cenceding (I); (2) identifying (MI) an agent that binds a polypeptide conclude is encoded by a coding sequence comprising a nucleotide sequence chosen from AEE31062, AEE31130, AEE31131, AEE311346, AEE31136, AEE31330, AEE31331, AEE31331, AEE31331, AEE31331, AEE31332, AEE31332, AEE31333, AEE31
                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polypeptide critical for survival of Haemophilus species, useful for reducing virulence of H. influenzae to be used as vaccine
                                                                                                                                                                                                 Gaps
distinguishing between functions of various members of a biological pathway. The present sequence is human haematopoietic cell tyrosine kinase antisense oligonucleotide
                                                                                                                                                                                                    ö
                                                                                                                                                    Length 20;
                                                                                                                                                                                                 Indels
                                                                                                                                               66.0%; Score 13.2; DB 10; 83.3%; Pred. No. 5.7e+03;
                                                                                              Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; antibacterial; trxB; PCR; primer; ss.
                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 121; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae trxB PCR primer.
                                                                                                                                                                                                                                              2 ACCGCATAGACTTCTCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arvidson
                                                                                                                                                                                                                                                                                20 AACTCATTGACTTCTCAG 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2005; 2005US-00194246
                                                                                                                                                                                                                                                                                                                                                                                         .152/c
AEE31152 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2006 (first entry)
                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOTT J E.
TREPOD C M.
ARVIDSON S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2006-037204/04
                                                                                                                                                                      Best Local Similarity
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Novel mutant protein tyrosine kinase-related oligonucleotide SeqID428

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Gaps

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63.0%; Score 12.6; DB 15; Length 19; 78.9%; Pred. No. 1.2e+04; ive 0; Mismatches 4; Indels (

Local Similarity 78.9 hes 15; Conservative

Matches

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Query Match

ADT00440 standard; DNA; 20 BP

RESULT 5 ADT00440

16-DEC-2004 (first entry)

ADT00440;

Sequence 19 BP; 6 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for atti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FES, GUCY2F and MCCK/MLK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity actimg as protein tyrosine kinase inhibitors or guanylate cyclase stimulators. The invention may be useful for developing methods for
                                                                                                                            tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
guanylate cyclase stimulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) an associated methods for diagnosing cancer and screening for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 428; 363pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bardelli A, Parsons W, Velculescu V,
                                                                                                                                                                                                                                                                                                                                          18-FEB-2004; 2004WO-US004452.
                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2003; 2003US-0448537P.
                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2003; 2003US-0473895P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-718702/70.
                                                                                                                                                                                                                                                                  WO2004082458-A2.
                                                                                                                                                                                                                              Ното варіеля
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Gaps

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Diagnosing hereditary hemochromatosis, involves providing sample comprising patient's nucleic acid, detecting presence or absence of A424G allele of polymorphism in nucleic acid that encodes transferrin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis and treatment of iron misregulation diseases including HFB bolypeptides and the polynucleotides encoding them. The iron misregulation diseases include both iron overload diseases and iron deficiency diseases. The invention is useful for diagnosing hereditary hemochromatosis and in gene therapy. The present sequence is human transferrin receptor (TFR) cDNA 424A allelle specific biotin-labeled oligonucleotide. This oligonucleotide is used in the screening for A424G polymorphism in the hereditary hemochromatosis patient chromosomes.
detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a human-derived oligonucleotide which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; pharmaceutical; iron overload; toxicity; intoxication; disorder of iron metabolism; hemochromatosis; cardiant; hepatotrophic; metabolic disorder; gene therapy; TFR; transferrin receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                 Human TFR cDNA 424A allele specific biotin-labeled 5' oligo, TFRdl.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to methods and compositions for the
                                                                                                      Length 20;
                                                                                                                                      Indels
                                                                                                  / Match 63.0%; Score 12.6; DB 13; Local Similarity 78.9%; Pred. No. 1.2e+04; He 15; Conservative 0; Mismatches 4;
                                                                  Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Biotin-labeled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/mod_base= OTHER
                                                                                                                                                                     1 GACCGCATAGACTTCTCAG 19
                                                                                                                                                                                           GACCCCGTAGTCATCTCAG 20
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97US-00834497.
97US-00866211.
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                                                                                                                                                                                                                                                                                  ADW95798 standard; DNA; 20
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modified_base
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04-APR-1997;
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                                                                                                    Query Match
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63.0%; Score 12.6; DB 14; Length 20; 78.9%; Pred. No. 1.2e+04;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of treating hemochromatosis in a patient by administering the hemochromatosis protein HFE (HLA-H) to the patient. The method is used for treating hemochromatosis. The invention provides a molecular basis for the relationship of HFE to iron metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of hemochromatosis in a patient involves administering HFE (HLA
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                               Human transferrin receptor OLA oligonucleotide TFRd1.G SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and diagnostic and therapeutic agents for the treatment of iron misregulation diseases. The present sequence represents an oligonucleotide ligation assay (OLA) oligonucleotide for the human transferin receptor, which is used in an example from the present
                                                                                                                                                                                                                         cardiant; hepatotropic; transferrin receptor; ss.
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Pred. No. 1.2e+04;
0; Mismatches 4;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; SEQ ID NO 12; 26pp; English
                          GACCGCATAGACTTCTCAG 19
                                                 2 GACAGACAGACTTCACCG 20
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    -H) polypeptide to the patient.

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97US-00866211.
97US-00920559.
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78.9%;
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                                                                                                                  ADZ44776 standard; DNA; 20
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                                                                                                                                                                    14-JUL-2005 (first entry
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Best Local Similarity 78.9
Matches 15, Conservative
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feder JN, Schatzman RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIRA ) BIO-RAD LAB INC.
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                                                                                                                                                                                                                         hemochromatosis;
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13-JUN-1997;
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                                                                                                                                                                                                                                                               Synthetic.
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DT 03-;
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                                                                                                      ADZ44776
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Necrosis factor kappa B (NFKB) sub-unit modulating DNAzyme, #56.

lung cancer; Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer; prostate cancer; colorectal cancer; brain cancer; osophageal cancer; stomach cancer; blader cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glloma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouraci; carboplatin; edarexate; gencitabine; radiation therapy; inflammatory disease; asthma; diabetes; restenosis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerubonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss. Synthetic. 

US2002177568-A1.

28-NOV-2002.

23-MAY-2001; 2001US-00864785

94US-00245466. 94US-00291932. 96US-00777916. 18-MAY-1994; 23-DEC-1996; 07-DEC-1992;

(STIN/) STINCHCOMB D T. (MCSW/) MCSWIGGEN J.

(DRAP/) DRAPER K G.

Draper KG; Mcswiggen J, Stinchcomb DT,

WPI; 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3; Page 46; 72pp; English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor rappa B (NPKB), where (I) is an inozyme, decleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, bepecially MG^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or unlitural resistant cancer. The method involves use of other drug cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or continuity resistant cancer. The method involves use of other drug charapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methorrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gencitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gencitabine or radiation therapy. The enzymatic and antisense uncleic acid molecules are also useful for treating inflammatory disease such as cyclophosphamic area also useful for treating inflammatory disease such as the control system (CNS) and myocardial), glomerulonephritis, sepansis, allergic airway inflammatory inflammatory bowel disease or infection. This sequence represents an enzymatic nucleic acid used to metrosis factor kappa B sub-unit

Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

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                          Gaps
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62.0%; Score 12.4; DB 8; Length 17; 64.3%; Pred. No. 1.5e+04;
                         1; Indels
                         4; Mismatches
            llarity 64.3%;
Conservative
        Local Similarity
nes 9; Conserv
Query Match
            Best Loca
Matches
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Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; d-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; broin cancer; colorectal cancer; brain cancer; colorectal cancer; pancreatic cancer; lessophageal cancer; teomach cancer; bladder cancer; pancreatic cancer; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic alrway inflammatory bowel disease; infection; ss.
                                                                                                                                                      NFKB sub-unit modulating inozyme substrate #499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Draper KG;
                                                                                  ACA06680 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-00987132.
94US-00245466.
94US-00291932.
96US-00777916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stinchcomb DT, Mcswiggen J,
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             CAUGGACTUCTICAG 17
CATAGACTICICAG 19
                                                                                                                             03-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-340953/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DRAP/) DRAPER K G.
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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23-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2002.
                                                                                                        ACA06680;
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Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3; Page 34; 72pp; English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG/2'+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edarrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic φ

ABT05045 standard; DNA; 18 BP

RESULT 11 ABT05045/

CGCCCAGTCTTCTCAGA

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acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CMS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
inflammation; tumour formation; TNFR1; anticancer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of tumor necrosis factor type 1 expression for and prevention of disease, particularly tumors.
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                                                                                                                                                                                                    Score 12.4; DB 8; Length 17;
Pred. No. 1.5e+04;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18942.
                                                                                                                                                               Sequence 17 BP; 4 A; 6 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                   Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      AAZ48549 Btandard; DNA; 18
                                                                                                                                                                                                                                                                            6 CATAGACTICICAG 19
                                                                                                                                                                                                                                                                                              2 CAUGGACUUCUCAG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowsert LM;
                                                                                                                             nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, treatment
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Novel antisense compound targeted to nucleic acid molecule encoding tumor necrosis factor receptor 1 (TNFR1), useful for treating humans having disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length targeted to nucleic acid molecule encoding tumour necrosis factor receptor 1 (TNFR1), where the antisense compound inhibiting the expression of TNFR1 in cells or tissues. The antisense compound is useful for inhibiting the expression of treating an animal (preferably human) having a disease or condition associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver injury) or a hyperproliferative disorder such as cancer, by inhibiting the expression of TNFR1. The antisense compound is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. This polymucleotide sequence represents a human oligonucleotide relating
                                                                                                                                 use compound; tumour necrosis factor receptor 1; liver disease; hepatitis; liver injury; hyperproliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antisense compound 8 to 30 nucleotides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                  TNFR1 expression modulation related antisense oligo SEQ ID No 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.0%; Score 12.2; DB 6; Length 18; 82.4%; Pred. No. 1.9e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TNFR1 antisense oligonucleotide segid 75.
                                                                                                                                                                                                                                                                                                                                                                                                      Dean NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 45; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the TNFR1 of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                  22-OCT-2001; 2001WO-US051224.
                                                                                                                                                                                                                                                                                                                                   24-OCT-2000; 2000US-00695451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CGCATAGACTTCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ceccaercrrcrcaea
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                                                                 (first entry)
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Baker BF, Cowsert LM,
                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-583481/62.
                                                                                                                                                                                                                                  WO200248168-A1.
                                                                                                                                                                                                   Homo sapiens.
                                                                 11-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-2004
                                                                                                                                                                                                                                                                   20-JUN-2002
                                                                                                                                 Antisense
                                                                                                                                                                      human; ds
                                ABT05045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR06077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                 TNFR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR06077/6
ID ADR06
XX
AC ADR00
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DT 21-00
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DE Human
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Gaps

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61.0%; Score 12.2; DB 3; Length 18; 82.4%; Pred. No. 1.9e+04; ive 0; Mismatches 3; Indels

4 CGCATAGACTTCTCAGA 20

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14; Conservative

Query Match Best Local Similarity Matches 14; Conserv

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Pseudomonas syringae pv. tomato DC3000 Hop gene PCR primer #40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL12249
110 ADL1
120 ADL1
120
    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting radiation-induced apoptosis in a cell or tissue comprises administering to the cell or tissue an antisense oligonucleotide targeted to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a method of inhibiting radiation-induced apoptosis in a cell or tissue an antistense oligonucleotide of 8-30 nucleotides in length targeted to a nucleic acid molecule encoding tumour necrosis factor receptor 1 (TNFR1). The method and antisense oligonucleotides are useful for inhibiting radiation-induced apoptosis in a cell or tissue, and for treating diseases associated with the expression of TNFR1. This sequence represents a human tumour necrosis factor receptor 1 (TNFR1) antisense oligonucleotide.
                cytostatic; gene therapy; apoptosis inhibitor; radiation-induced apoptosis; tumour necrosis factor receptor 1; INFR1; human; antisense oligonucleotide; antisense technology; ss.
                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                            /note= "OTHER= Optionally 2'-0-Methoxyethyl (2'-MOB)
nucleotides"
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                                                                                                                                                                                                                  'note= "OTHER= Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.2; DB 13;
Pred. No. 1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; SEQ ID NO 75; 24pp; English.
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                          base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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17-JUN-1999; 99WO-US013763.
24-OCT-2000; 2000US-00695451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 61.0%;
1 Similarity 82.4%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCCAGTCTTCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CGCATAGACTTCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG73193 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                     15. .18
                                                                                                                                                                                                                                                     *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004147471-A1
                                                                                                                                    Key
modified_base
                                                                                                                                                                                                                                                                                                                                   modified base
                                                                                                                                                                                                                                 modified_base
                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG73193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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New nucleic acid, useful in imparting disease resistance to a plant or in preparing a composition for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pv. tomato DC3000 Avr/Hop proteins, and the polynucleotide sequences canceding them. Also disclosed are expression vectors, host cells, and transgenic plants comprising polynucleotide sequences of the invention. The polynucleotide and polypeptide sequences are useful in imparting disease resistance to a plant or in preparing a composition for treating cancer. The sequences may also be used to make a plant hypersusceptible to colonisation by nonpathogenic bacterial modify a metabolic pathway in a cell, cause enkaryotic cell death, and inhibit programmed cell death. The present sequence represents a PCR primer used in the examples of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to the isolation of Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Avr; Hop; transgenic plant; disease resistance; cancer; bacteria; metabolic pathway; eukaryotic cell death; programmed cell death;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cartinhour SW, Schneider DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; Avr; Hop; cancer; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.2; DB 10;
Pred. No. 1.9e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae anti-cancer gene primer #60.
                                                                                                            Pseudomonas syringae; pv. tomato str. DC3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCATAGACCTGTCTG 19
                                                                                                                                                                                                                                                                         12-FEB-2003; 2003US-00365742.
                                                                                                                                                                                                                                                                                                                               12-FEB-2002; 2002US-0356408P.
10-MAY-2002; 2002US-0380185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.0%;
                                                      cytostatic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                               COLLMER A.
ALFANO J R.
CARTINHOUR S W.
SCHNEIDER D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collmer A, Alfano JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-875735/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
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                                                                                                                                                               US2003204868-A1
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                                                                                                                                                                                                                     30-OCT-2003
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(SCHN/)
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Search completed: June
Job time : 293 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMG-COA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding HMG-COA reductase, useful for treating atherosclerosis, or a disease involving cholesterol metabolism or
                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule, useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID No 389
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0
                                                                                                                                                                                                                                                                                                             Tang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 61.0%; Score 12.2; DB 10; Length 19; Local Similarity 82.4%; Pred. No. 1.9e+04; les 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                             Schneider DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 187; 284pp; English.
                                                                                                                                                                                                                                                                                                             Cartinhour SW,
                                                                                                                                                                                           (USDA ) US SEC OF AGRIC.
(UYNE-) UNIV NEBRASKA.
(UNIV ) UNIV KANSAS STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dobie KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCGCATAGACTICTCAG 19
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                               12-FEB-2003; 2003WO-US004450.
                                                                                                                                                                  CORR ) CORNELL RES FOUND INC
                                                                                  12-FEB-2002; 2002US-0356408P.
10-MAY-2002; 2002US-0380185P.
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                                                                                                                                                                                                                                                                                                       Collmer A, Alfano JR,
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                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-679632/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-081743/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004006031-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention
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                                                                     The invention relates to novel compounds of 8-80 nucleobases in length targeted to, and which specifically hybridises with, a nucleic acid molecule encoding 3-bydroxy-3-methylglutary1-Consyme A (HMG-COA) reductase, and inhibits the expression of HMG-COA reductase. The novel compounds have cardiant, antiarteriosclerotic, and antilipaemic activities. The compound can be used to treat disorders by antisense gene therapy. The compounds compositions and methods are useful for treating a disease or condition associated with HMG-COA reductase, such as a cardiovascular disorder e.g. atherosclerosis, or a disease or condition involving cholesterol metabolism. They are also useful in research and diagnostics for modulating the expression of HMG-COA reductase. This polymucleotide sequence represents an antisense oligonucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 12.2; DB 12; Length 20; 82.4%; Pred. No. 1.9e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Example 16; SEQ ID NO 389; 110pp; English.
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Best Local Similarity 82.4
Matches 14; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz50445 BST R0050	Adu41462 Knock-dow	Adi85951 Nucleic a	Aaz05689 PCR prime	Aec30315 Human loc	Aac63691 Rat P2X 7	Ada09833 Antisense	Aav97668 Human EGF	Adi85562 Nucleic a	Adk96254 Primer of	Adf50105 Human BCL	Adf50117 Human BCL	Adf50125 Human BCL	Adf50109 Human BCL	Adg29696 BCL2-tard	Adq29693 BCL2-targ	Adg29700 BCL2-targ	
SUMMARIES	QI	AAZ50445	ADU41462	ADJ85951	AAZ05689	AEC30315	AAC63691	ADA09833	AAV97668	ADJ85562	ADK96254	ADF50105	ADF50117	ADF50125	ADF50109	ADG29696	ADG29693	ADG29700	ADV65888
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de	Query Match	100.0	66.7	65.7	64.8	62.9	61.9	61.9	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0
	Score	21	14	13.8	13.6	13.2	13	13	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8
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				ACL49849 ACL49849 HAVCRI ta														Ady21139 Human	Aaq51964 BCL-2 a Aav97667 Human l	ALIGNMENTS							PC; chromosome 11p11.1-11	mechanism; e potential; n	ck pitmer; ss.						W SERVICES.	LA;		ed in prostate cancer useful for diagnosing	sh.	ST AAR00504-specific PCR primer, used for trained within the EST AAR00504. It is expressed in prostate cancer epithelium and expession of the EST. The PB39 gene that is it is isolated from human pancreas cDNA
2 2	12	77	7 5	14	26 12.4 59.0 21 14 ACLA 27 12.4 59.0 21 14 ACLA 28 12.2 58.1 17 2 AAV9 29 12.2 58.1 17 2 AAV9 29 12.2 58.1 17 2 AAV9 29 12.2 58.1 20 2 AAV9 31 12.2 58.1 20 12 ADP8 33 12.2 58.1 20 12 ADP8 34 12.2 58.1 20 12 ADP8 35 12 57.1 20 12 ADP8 39 12.2 58.1 20 12 ADP8 39 12 57.1 20 14 ADV9 41 12 57.1 20 14 ADV9 42 12 57.1 20 14 ADV9 43 12 57.1 20 14 ADV9 44 12 57.1 21 13 AER8 44 11.8 56.2 17 2 AAV99 45 11.8 56.2 17 2 AAV99 46 12 57.1 21 14 ADV9 47 11.8 56.2 17 2 AAV99 48 56.2 17 2 AAV99 49 56.2 17 2 AAV99 40 12 57.1 21 4 ABV9 40 12 57.1 21 14 ADV9 41 11.8 56.2 17 2 AAV99 42 11.8 56.2 17 2 AAV99 43 12 57.1 21 14 ADV9 44 11.8 56.2 17 2 AAV99 45 11.8 56.2 17 2 AAV99 46 12 57.1 21 14 ABV9 47 11.8 56.2 17 2 AAV99 48 56.2 17 2 AAV99 49 56.2 17 2 AAV99 40 56.2 17 2 AAV99 40 600005376-A1. 40 600005376-A1. 41 600005376-A1. 42 600005376-A1. 43 11.8 56.2 17 2 AAV99 44 11.8 56.2 17 2 AAV99 45 11.8 56.2 17 2 AAV99 46 12 57.1 21 4 AAV9 47 10.999; 99WO-US016831. 48 50.2 10.00005376-A1. 49 600005376-A1. 40 600005376-A1. 40 600005376-A1. 40 600005376-A1. 41 600005376-A1. 42 600005376-A1. 43 600005376-A1. 44 600005376-A1. 45 600005376-A1. 46 600005376-A1. 47 600005376-A1. 48 600005376-A1. 48 600005376-A1. 49 600005376-A1. 40 6000005376-A1. 40 6000005376-A1. 40 600000000000000000000000000000000000																																			
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restriction endonuclease site; T3 promoter site; Tag gene; Poly A site, T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control; assay development; product development; product validation;
                                                                                                                              Nucleic acid analysis-related Tag probe SeqID1019.
                                               ADJ85951 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                    14-JUL-2003; 2003WO-US021990.
                                                                                                                                                                                                                                                                                                                                               12-JUL-2002; 2002US-0395530P.
                                                                                                                                                                                                quality control; probe; ss
                                                                                                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                WO2004007684-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    Christians FC;
                                                                                                                                                                                                                         Synthetic.
Unidentified.
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                                                                          ADJ85951;
                                    ADJ85951/c
                      RESULT 3
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library and has homology to the EST AAR00504. PB39 gene is located on chromosome llpl1.1-11.2. Abnormally high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of precancerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of differing aggressiveness and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a polynucleotide comprising an RNA sequence. The polynucleotides, vector, libraries, and method are useful in lowering the amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New knockdown sequences, useful in lowering the amount of RNA and/or protein production in cells used in drug development process.
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                                                                                                                                                                               Score 21; DB 3; Length 21; Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; RNA production; protein production; drug development;
                                                                                                                                                                                                          0; Indels
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                                                                                                                                                    Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 6678; 402pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                Knock-down target sequence #6641.
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                                                                                                                                                                           ch 100.0%;
11 Similarity 100.0%;
21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GALA-) GALAPAGOS GENOMICS NV (VSCH/) VAN DER SCHUEREN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2003; 2003WO-EP004362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2003; 2003WO-EP004362
                                                                                                                                                                                                                                                                                                                                ADU41462 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arts GJF, Lambrecht MJY,
Griffioen S, Bergs CJL;
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                           metastatic potential
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Matches 14; Conserv
                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       knock-down target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004094636-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                          ADU41462;
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Matches
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ADU41462/c
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                                                           New DNA molecules made by annealing and extending overlapping 60mer oligonuclectides, useful in producing synthetic Tag genes useful as assay controls, in assay development, product development and for quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.7%; Score 13.8; DB 12;
88.2%; Pred. No. 4.1e+03;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                               Disclosure; SEQ ID NO 1019; 91pp; English.
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nes 15; Conservative
WPI; 2004-122923/12.
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Gaps

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TGGCGTATCTGAAG 15

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Conservative

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                 Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAX36754-X37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal untertitis, pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haplotype mapping; genetic marker; single nucleotide polymorphism; SNP; major histocompatibility complex; MHC; HLA; human leukocyte antigen; manune disorder; inflammation; inflammatory bowel disease; ulcerative colitis; Crohns disease; rheumatoid arthritis; diabetes; diabetes mellitus; mysthenia gravis; vitiligo; Graves disease; Hashimotos disease; Addison's disease; gastritis; autoimmune hepatitis; rheumatism; spetemic lupus erythematosus; scleroderma; polymyositis; dermatomyositis; pernicious anemia; primary biliary cirrhosis; idiopathic thrombocytopenia purpura; Sjoegrens syndrome; multiple sclerosis; Reiter's syndrome; psoriasis; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.6; DB 2; Length 20;
Pred. No. 5.2e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human locus-specific oligonucleotide #1603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 1791; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TGGCGTATCTGAAGAGTCTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 TGTCGTTTCAGAAGAGGCTG 1
                                                                                                                                                                                                                                                                                 97FR-00015041.
97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                 98WO-IB001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 64.8%;
1 Similarity 80.0%;
16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                  Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                    WO9928475-A2
                                                                                                                                                                                                                                               27-NOV-1998;
                                                                                                                                                                                                                                                                                                         17-DEC-1997;
04-NOV-1998;
                                                                                                                                                                                                                                                                                     28-NOV-1997;
                                                                                                                                                                                                          10-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                    Griffais R;
                                                                                                               Synthetic
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ID AEC30315/C
XX
AC AEC3033
XX
XX
DT 17-NOV
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XX
Mulcarat
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The invention relates to a method of identifying the nucleotide for each of a set of single nucleotide polymorphisms (SNPB) in the major histocompatibility complex (MRC) region in a population of individuals, comprising the HLA type for the individuals and identifying an SNP haplotype in the population that correlates with the HLA type, where the SNPB haplotype comprises the SNPB in the MHC region. The invention also relates to a method of predicting the HLA type of an individual, a method of determining the presence or absence of an individual, a method of identifying an SNP haplotype that correlates with susceptibility to a disease or condition, and a method of determining the susceptibility of a disease or condition. The disease or condition is an individual to a disease or condition. The disease or condition is an individual to a disease or condition selected from inflammatory bowel disease, ulcerative colitis, condition selected from inflammatory bowel disease, disease, adisease, adisease, attendates mellitus, mysathenia gravis, vitiligo, Graves disease, Hashimoto's disease, Addison's disease, systemic selectosis, polymositis, dermatomyositis, dermatomyositis, permicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia purpura, Sjoegren's syndrome, multiple sclerosis, Reiter's syndrome and primary bloomed in the sequence represents a human locus-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; P2X_7; neuroprotective; nootropic; antiinflammatory; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
gastrointestinal-gen.; antiulcer; immunomodulator; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; muscular-gen.; neuroprotective; dermatological; antithyroid; hepatotropic; antianemic; hemostatic; ophthalmological; uropathic; antipsoriatic; ss; SNP detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying single nucleotide polymorphism (SNP) haplotype that correlates with the HIA type, useful for diagnosing an immunological inflammatory condition, comprises providing SNPs in the major histocompatability complex region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 8.4e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 6335; 175pp; English.
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                                                                                                                                                                                                                                             28-FEB-2005; 2005WO-US006628.
                                                                                                                                                                                                                                                                                     26-FEB-2004; 2004US-0547823P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat P2X_7/P2Z PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 CTGGGGTATATGGAGAGT
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Oliphant A, Murray S;
                                                                                                                                                                                                                                                                                                                           (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-638856/65.
                                                                                                                                                               WO2005082110-A2.
                                                                                                                       Homo sapiens
                                                                                                                                                                                                     09-SEP-2005.
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lymphoproliferative disorder; apoptosis; ischaemia; rat;

autoimmune disorder

JS6509163-B1

Rattus sp.

21-JAN-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to rat and human purinergic receptor PZX_7/PZZ (AAC53693-C63694). The PZX_7 coding sequences can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's disease, diseases involving acute or chronic inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the haematopoietic system and immune response such as autoimmune disorders, allergies and lymphoproliferative disorders, diseases involving apoptotic cell death, such as cardiac and cerebral ischaemia and microbial infections, particularly tuberculosis. The present sequence is a PCR primer used to isolate the rat PZX_7 coding sequence
antiarthritic; antibacterial; antiviral; antiallergic; cytostatic; cardiant; cerebroprotective; immunosuppressive; PZZ; purinergic receptor; nervous system disorder; chronic inflammation; Alzheimer's disease; rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection; hammatopotatic system disorder; immune response; autoimmune disorder; allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia; tuberculosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. -
                                                                                                                                                                                                                                                                                                                                       Surprenant A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                   (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                     Kawashima E,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-006153/01.
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                                                                                                                                                                                                                                                                    28-APR-1997;
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                                                                                                                                                                  US6133434-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodies.
                                                                                                                                  Rattus sp.
                                                                                                                                                                                                                                                                                                                                    Buell GN,
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Screening of compound for its ability to modulate permeabilizing activity of mammalian receptor useful for treating e.g. arthritis, and alzheimer's

Example 1; SEQ ID NO 3; 43pp; English.

disease

Kawashima E;

Buell GN, Surprenant A,

WPI; 2003-502654/47.

(GLAX ) GLAXO GROUP LTD

15-AUG-2000; 2000US-00638857.

97US-00842079.

28-APR-1997;

The invention discloses a method for screening a compound for its ability receptor. The P2Z receptor is a cell surface receptor for ATP and has been implicated in the lysis of antigen presenting cells by cytotoxic T lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well as in the formation of multinucleated giant cells. The preferred agonist is adenosine triphosphate (ATP) or 3,-0-(4-benzoyl)benzoyl ATP (BZATP) and the preferred method comprises monitoring the uptake into the cell of

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                                                                                                                                                                                                                                                                                                                                                                                                                                             and cue presented method complishes monitoring une upract into the control of an electable molecule, preferably a fluorescent dye (e.g. propidium iodide). The inventive method is useful for screening a compound for its ability to modulate the permeabilishing activity of a mammalian P2X7 receptor useful for treatment of arthritic and respiratory disorders and neurodegenerative diseases. It is particularly useful in the treatment of Alzheimer's diseases, diseases involving acute or chronic inflammation including rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, e.g. tuberculosis, disorders of the haematopoietic system and immune response, including autoimmune disorders, allergies and such as cardiac and cerebral ischaemia. The sequence presented is a nested for the amplification of rat P2X7 CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, epidermal growth factor receptor; EGPR; EGP-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13; DB 9;
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1es 13; Conservative
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PCR; ss; primer; permeabilising activity; P2X7 receptor; P2Z receptor; receptor: ATP; antigen presenting cell; T lymphocyte; mitogenic stimulation; multinucleated giant cell; adenosine triphosphate; 3'-0-(4-benzoyl) benzoyl ATP; BAXTP; [luorescent dye; propidium iodide; nootropic; neuroprotective; immunosuppressive; cerebroprotective; vasocropic; arthritic disorder; respiratory disorder; neurodegenerative disease; Alzheimer's disease; inflammation; rheumatoid arthritis; amyloidosis; infection; tuberculosis; haematopoietic system; immune response; allergy;

Antisense nested PCR primer #1 for amplification of rat P2X7 (P2Z).

WO9833893-A2

06-AUG-1998

14-JAN-1998; 31-JAN-1997; 04-DEC-1997;

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Akhtar

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This invention relates to a novel DNA molecule which comprises a DNA molecule made up of the following elements in a 5' to 3' direction: a first restriction endonuclease site; a T3 promocter site; at least one Tag gene comprising at least 5 20mer Tag sequences; a Poly A site having at least 21 consecutive A residues; a second restriction endonuclease site which may be the same or different than the first restriction endonuclease site; or a T7 Promoter on the opposite strand as the T3 promoter. The invention may be useful in nucleic acid analysis, in particular to synthetic Tag genes useful as assay controls, in assay development product development and validation and for quality control. The present sequence is that of a Tag oligonucleotide probe which may be used during the creation of the novel DNA molecule of the invention.
                                                                                                                    New DNA molecules made by annealing and extending overlapping 60mer oligonuclectides, useful in producing synthetic Tag genes useful as assay controls, in assay development, product development and for quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a polynucleotide isolated from a human gene and is useful for detecting a single nucleotide polymorphism in a human gene or for diagnosing of disease. The invention enables the detection of a single nucleotide polymorphism in a human gene. The present sequence represents a primer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.0%; Score 12.8; DB 12; Length 20; 87.5%; Pred. No. 1.3e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; single nucleotide polymorphism; SNP; ss; primer.
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                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 630; 91pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer of the invention #1974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GCGTATCTGAAGAGTC 19
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Les 14; Conservative
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                                                          WPI; 2004-122923/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes enzymatic nucleic acid molecules (NAMS) which specifically cleave RNA derived from an epidermal growth factor receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98866 and AAV98867 to V9978 represent hammerhead ribozymes and hairpin ribozymes respectively for human EGF-R. The NAMS are useful for cleaving EGF-R RNA in the treatment of a condition associated with EGFR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMS can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of EGF-R RNA in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ic nucleic acids - which cleave RNA derived from an epidermal factor receptor, useful for inhibiting cell proliferation and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction endonuclease site; T3 promoter site; Tag gene; Poly A site; T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control; assay development; product development; product validation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 77; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen JA
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ID ADJUBS562 standard; DNA; 20 BP. XX
AC ADJUBS562;
XX
C ADJUBS562;
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C ADJUBS562;
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DE Nucleic acid analysis-related TaXX
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TO Fromoter; nucleic acid analys
XM restriction endomuclease site; T
XM assay development; product 
                                                                                                                 98WO-US000730.
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                        88; 81NA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
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                             Query Match 61.0%; Score 12.8; DB 12; Length 20; Best Local Similarity 87.5%; Pred. No. 1.3e+04; Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                        Human BCL2 siNA target sequence SEQ ID NO:833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; SEQ ID NO 833; 148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2002US-0358580P.
; 2002US-0363124P.
; 2002US-0386782P.
; 2002US-0396905P.
; 2002US-0406784P.
; 2002US-0406378P.
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15-JAN-2003; 2003US-0440129P
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                                                                                                                                                                                                                      ADF50105 standard; RNA; 21
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                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                    1 CTGGCGTATCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-712622/67.
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29-AUG-2002;
05-SEP-2002;
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11-MAR-2002;
06-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNA of the invention has cytostatic, immunosuppression, vircide, and anti-HIV activity. The siNA are useful for modulation (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacognomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
                                                                                                                                                                                                                                    ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
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87.5%; Pred. No. 1.4e+04;
tive 0; Mismatches 2;
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                                                                                                                                                                                                        Human BCL2 siNA target sequence SEQ ID NO:845.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2002; 2002US-0353124F.
06-UTM-2002; 2002US-0386782P.
18-UTL-2002; 2002US-0396905F.
29-AUG-2002; 2002US-0406784P.
05-SFP-2002; 2002US-0408378P.
15-JAN-2003; 2003US-0440129P.
                                                                                                          ADF50117 standard; RNA; 21 BP
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GTATCTGAAGAGTCTG
                                                                                                                                                                          (first entry)
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nes 14; Conservative
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61.0%; Score 12.8; DB 10; Length 21; 56.2%; Pred. No. 1.4e+04; ive 5; Mismatches 2; Indels C

Query Match
Best Local Similarity 56.2
Matches 9; Conservative

ADP50125;

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The invention relates to a novel short interfering nucleic acid (siNA) that downregulates expression of the BCL2 gene by RNA interference. A siNa of the invention has cytostatic, immunosuppression, virucide, and anti-HIV activity. The siNA are useful for modulateon (inhibition) of expression or activity of BCL2 by RNA interference. siNA are used to modulate expression of BCL2 genes, in cells, tissue explants or organisms, e.g. for treating cancer, autoimmune diseases and viral infections (including by HIV) but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
                                                                  ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer or autoimmune disease, downregulates expression of the BCL2 gene.
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                                 Human BCL2 siNA target sequence SEQ ID NO:837.
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2002US-0386782P.
2002US-0396905P.
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2002US-0408378P.
2002US-0409293P.
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les 14; Conservative
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05-SEP-2002;
09-SEP-2002;
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                                                                                                                                                                                         88; 81NA; human; BCL2; short interfering nucleic acid; RNA interference; cytostatic; immunosuppressive; virucide; anti-HIV; cancer; autoimmune disease; viral infection; HIV.
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                                                                                                                                                 Human BCL2 siNA target sequence SEQ ID NO:853.
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11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0366782P.
18-JUL-2002; 2002US-0396905P.
29-AUG-2002; 2002US-0406784P.
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ADF50109 standard; RNA; 21 BP.
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ADP50125/c
ID ADP50125 standard; RNA; 21
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                                                                                                          (first entry)
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Matches 14; Conservative
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Query Match

8 셤 ADF50109;

ADP50109/c
ID ADP5(
XX
AC ADP5(
XX

RESULT 14

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The invention relates to a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene comparish one or more chemical modifications and each strand of the double-stranded siNA comprises about 21 nucleotides. The siNA of the invention demonstrates antiarteriosclerotic, neuroprotective, cot the invention demonstrates antiarteriosclerotic, neuroprotective, cootropic, antiparkinsonian and anticonvulsant activities and may be useful for down-regulating the expression of an endogenous mammalian target gene and therefore in the treatment of any disease or condition target gene and therefore in the treatment of any disease or condition tissue or organism. The disease or condition may include pulmonary disease such as restenois, atherosclerosis, Alzheimer's disease, Parkinson's disease, epilepsy, dementia, huntington's disease or amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for gene therapy applications. The current sequence is that of the siNA DNA-RNA bybrid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New double-stranded short interfering nucleic acid molecule, useful for down-regulating the expression of an endogenous mammalian target gene or for treating diseases that respond to modulation of gene expression or activity.
Alzheimer's; Parkinson's; epilepsy; dementia; huntington's; amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chowrira B, Pavco P, Fosnaugh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 3 A; 5 C; 5 G; 2 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 24; SEQ ID NO 262; 593pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beigelman L, Chowr
man N, Thompson J;
                                                                                                                                                                                                                                              20-FEB-2002; 2002US-0358580P.
11-MAR-2002; 2002US-0363124P.
06-UTM-2002; 2002US-0386782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2003US-040929P.
15-JAN-2003; 2003US-0440129P.
                                                                                                                                                                                                                                                                                                                                                                                                                    (SIRN-) SIRNA THERAPEUTICS INC
                                                                                                                                                                                                          20-FEB-2003; 2003WO-US005028
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcswiggen J, Вездеты
----- S. Usman N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-731676/69.
                                                                                                                          WO2003074654-A2.
                                                            Unidentified
                                                                                                                                                                   12-SEP-2003
                                                                                     Synthetic.
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61.0%; Score 12.8; DB 10; Length 21; 56.2%; Pred. No. 1.4e+04; ive 5; Mismatches 2; Indels C 6 GTATCTGAAGAGTCTG 21 9; Conservative Local Similarity Matches ઠ

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Search completed: June 9, 2006, 00:12:32 Job time: 290 secs

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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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22
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz50444 BST R0050	Aax96007 PCR prime		Aca92364 Lawsonia	Adq33930 L. intrac	Adj66835 Lawsonia	Adr72987 Lawsonia	Aeb18062 L. intrac	Aaf85459 Polynucle	Aec52046 Antisense	Aec51906 Antisense	Aec51766 Antisense	Aaa60336 Human HPC	Aas99071 Human pro	Aat33010 Mouse SRY	Abk87666 Synthetic	Ada66516 Transform	Adg89282 Cancer de
SUMMARIES	а	AAZ50444	AAX96007	AAI98006	ACA92364	ADG33930	ADJ66835	ADR72987	AEB18062	AAF85459	AEC52046	AEC51906	ABC51766	AAA60336	AAS99071	AAT33010	ABK87666	ADA66516	ADG89282
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,	Query Match	100.0	69.1	60.0	0.09	0.09	60.0	60.0	60.0	59.1	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.2
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Adp27751 PCR prime Adr00153 COX2 prob	Adw45702 Adw72150	Adw73436 Human B7	Adw73461 Adq13916	Adx03606	Ady96387 Ady98415	Ady98302 e1F4E Adv98416 Eukarv	Ady 03829	Aea34557 Aea44481	Add18145 Human	Adi41032 Human	Aag61732	Aat27443		Abn89231	Adg90494 Human Adc65754 Humar	Adf90932 Microo Abz86479 Human	ENTS						chromosome llpll.1-11.2; cancer; anism; early diagnosis; progression; ntial; non-neoplastic prostate disease; rimer; ss.						BS.			in prostate cancer useful for diagnosing		ence is the BST AAR00504-specific PCR primer, used for sequences contained within the BST AAR00504. It is the gene overexpressed in prostate cancer epithelium and ifferential expression of the BST. The PB39 gene that is prostate cancer is isolated from human pancreas cDNA
ADP27751 ADR00153	ADW45702 ADW72150	ADW73436	ADW73461 ADQ13916	ADX03606	ADY98415	ADY98302 ADY98416	ADY03829	AEA34557 AEA44481	ADD18145	ADI41032	AAQ61732	AAT27443	AAZ70423	ABN89231	ADG90494 ADC65754	ADF90932 ABZ86479	ALIGNMENTS		BP.			:	PC; mech pote				•		AN SERVICES	a LA;			English.	the EST AAR00504-sp is contained within overexpressed in p al expression of the cancer is isolated
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21	217	13	20	200	202	200	19	19	50	202	18	18	18	20	0 0	50 50 50			DNA;		t entry)	c primer	870.8				9WO-US016831	98US-0094137	DEPT HEALTH &	KA,		is dysregulated	51pp; 1	equence is the cof sequences the gene over the gene over the differential in prostate ca
44	9.5	m, r	i ui	ų,	. n.	m m	4.	4. 4.	4	4. 4	'n	rvi n	u ru	ri.	v. v.	ri ri			standard;		(first	-specific	rost eliu				994	186	H	Cole	82700/16		16;	sequence on of sequence cobe the cope the different in prost
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12.		25	22.	12.	12.	12.	12.	12.	12.									H	444 AAZ50444	AAZ50444	-MAY-2000	T R00504	PB39; human; prostate of prostate epithelium; sprecancerous cell; metexpressed sequence tag	Homo sapiens	WO200005376	-FEB	-JUL-1	-JUL-1	( HSSU)	Chuaqui	1; 2000	Novel gene cancer.	Claim 5;	pre Lifi Eul anal regu
19	21	23	2 2	26	28	30	31	3 8	34	36	37	38	4 0	41	4 4 7 8	44			44 A	¥	18	EST	E T T T T T T T T T T T T T T T T T T T	HO	Š.	03	23	24	Đ	ទី	WPI;	N O B	บี	The amp used to a dys
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library and has homology to the EST AAR00504. PB39 gene is located on chromosome lipli.1-11.2. Abnormally high concentrations of PB39 are found in prostate tissue derived from prostate cancer (PC) epithelium. PB39 sequence is useful for detection of precancerous or cancer cells in the prostate. PB39 is useful for early diagnosis of the progression of prostate cancer, especially in aggressive prostate carcinoma. It can also distinguish PC from other non-neoplastic prostate disease. The diagnostic method is selective and specific for various types of PC and also facilitates identifying prostate cancer of differing aggressiveness and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis: The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34884 - AAX35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                   Score 22; DB 3; Length 22;
Pred. No. 0.6;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                 Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 1792; Disclosure; 1912pp; English
                                                                                                                                                                                                                                                                                                                                  GCATGTTACAGGTAGAAAAGCC 22
                                                                                                                                                                                                                                                                                                        1 GCATGTTACAGGTAGAAAGCC 22
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1 Similarity 100.0%; P:
22; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydophila pneumoniae.
                                                                                                                                                                  metastatic potential
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                                                                                                                                                                                                                                                     Best Loca
Matches
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AAX96007/
   8899999999988
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69.1%; Score 15.2; DB 2; Length 20;

Query Match

Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                      HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
                                                                                                                                                                                                                           Lawsonia intracellularis protein related oligonucleotide SEQ ID NO: 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer; 88; antibacterial; HtrA; PonA; HypC; Ly8S; YcfW; ABC1; Omp100; Lawsonia intracellularis infection; Orf1; pig; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides isolated polynucleotides encoding HtrA
                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawsonia intracellularis polynucleotide and encoded protein, used to prevent Lawsonia intracellularis infection.
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               Indels
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Pred. No. 1.4e+03;
); Mismatches 3;
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0
                                                                    20 GCCTGTTCCAGATAGAAAG 1
                                                                                                                                                                                                                                                                     vaccine; PCR primer; probe; ss.
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             17; Conservative
                                                                                                                                                                                                                                                                                             Lawsonia intracellularis
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Best Local Similarity
Matches 17; Conserv
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22-OCT-1999; 99US-0160922P.
05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
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(PFIZ ) PFIZER PROD INC.
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                                                                                   (ROSE/) ROSEY E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1999;
05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polynucleotide molecule comprising a sequence encoding Lawsonia intracellularis HtrA, PonA, HypC, Lyus, YcfW, ABC1 or Compilo protein. The invention also relates to a genetic construct comprising a polynucleotide molecule that can be used to alter a Lawsonia gene, comprising a polynucleotide molecule comprising a sequence that is otherwise the same as a nucleotide sequence of a htrA, ponA, hypC, lysS, ycfW, abc1 or omp100 gene, or its homologue, a substantial portion, or contactions capable of altering the above mentioned genes or a polynucleotide molecule comprising a sequence that naturally flanks in the ORP of the htrA, ponA, hypC, lysS, ycfW, abc1 or omp100 gene or its homologue. The invention also relates to a fusion protein of a polypeptide of the invention fused to another polypeptide or an analogue or derivative. The invention fuster relates to a substantially pure polypeptide comprising an epitope of HtrA, ponA, HypC, LysS, YcfW, ABC1 or Omp100 protein that is specifically reactive with anti-Lawsonia antibodies. The methods and compositions of the present invention are useful for the prevention and diagnosis of L. intracellularis infections in susceptible animals, such as pigs. Sequences ACA92134-ACA92415

C proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                        New isolated Lawsonia intracellularis polymucleotide and polypeptide, useful for the prevention and diagnosis of Lawsonia infections in susceptible animals, such as pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawsonia intracellularis; HtrA; PonA; HypC; LysS; YcfW; ABC1; Ompl00; pig; 88; sequencing; primer.
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Pred. No. 1.4e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

    L. intracellularis sequencing primer #26.

                                                                                                                                                                                                                                                                                                                               Example 2; Page 46; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TGTTACAGGTAGAAAGC 21
                                             01-AUG-2002; 2002US-00210296.
                                                                              22-OCT-1999; 99US-0160922P.
05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-2003; 2003US-00449462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG33930 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.0°
Best Local Similarity 83.3°
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawsonia intracellularis
                                                                                                                                                                                                                       WPI; 2003-416977/39
                                                                                                                                                   (ROSE/) ROSEY E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003202983-A1
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            30-JAN-2003
                                                                                                                                                                                       Rosey EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG33930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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The invention relates to a new isolated polynucleotide molecule which encodes Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein. The methods and compositions of the present invention are useful for the prevention and diagnosis of L. intracellularis infections in susceptible animals, such as pigs. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; vaccine; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; diagnostic agent; infection; pig; porcine proliferative enteropathy; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Lawsonia intracellularis polypeptides, useful as vaccines, as diagnostic agents, or in preventing infections in susceptible animals such as pigs, e.g. porcine proliferative enteropathy.
New isolated Lawsonia intracellularis polynucleotide and polypeptide, useful for the prevention and diagnosis of Lawsonia infections in susceptible animals, such as pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 13.2; DB 10; Length 21; 83.3%; Pred. No. 1.4e+04; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawsonia intracellularis PCR primer SegID50.
                                                                                                                                                       Example 2; SEQ ID NO 50; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 50; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGGTACAGCAAGAAAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TGTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0160922P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ66835 standard; DNA; 21
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gastrointestinal-gen.; gastrointestinal disease; HtrA; PonA; HypC; Orfl; primer; ss.
                                                                                                                                                                                                         L. intracellularis gene cluster B sequencing primer, ER178,
                                                                                       AEB18062 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999; 99US-0160922P.
05-NOV-1999; 99US-0163858P.
12-OCT-2000; 2000US-00689065.
                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2003; 2003US-00449648
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                           Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROSE/) ROSEY E L.
                                                                                                                                                                                                                                                                                                                                                             US2005143561-A1.
                                                                                                                                                                  08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosey EL;
                                                                                                                           AEB18062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                         ö
This invention relates to a novel isolated polypeptide derived from Lawsonia intracellularis. The invention may be useful for the development of compounds with an antibacterial activity or a vaccine. Specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawsonia intracellularis proteins: HtrA, PonA, HypC, LysS, Ycfw, ABC1, and Ompl00. The DNA and protein sequences of the invention are useful for preventing Lawsonia intracellularis infection of animals (e.g. pig). The present DNA sequence was used in the exemplification of the invention. NOTE: The present sequence is not shown in the specification but was obtained from the Japanese Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HtrA; PonA; HypC; Ly8S; YcfW; ABC1; Omp100; infection; primer; probe; 88.
                                                          claimed are L intracellularis proteins, such as Htth, Pond, HypC, LysS, Ycfw, ABCl and Omploo proteins. The invention may be useful for the development of vaccines, diagnostic agents, or in preventing L intracellularis infections in susceptible animals such as pigs, for example porcine proliferative enteropathy. The present sequence is that of a PCR primer which was used for amplification and/or sequencing of a region of L intracellularis DNA during the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polynucleotide comprising Lawsonia intracellularis nucleotide sequence that encodes HtrA, PonA, HypC, LysS, YcfW, ABC1 or Ompl00 protein or its essential portion, useful as diagnostic agent.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequences of the
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                              60.0%; Score 13.2; DB 10; Length 21; 83.3%; Pred. No. 1.4e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.2; DB 13; Length 21;
Pred. No. 1.4e+04;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                     Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lawsonia intracellularis DNA sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 50; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                regracaccaacaaaaacc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1999; 99US-0160922P.
20-OCT-2000; 2000JP-00320736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2004; 2004JP-00092095
                                                                                                                                                                                                                                                                                                ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                         4 TGTTACAGGTAGAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR72987 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-597336/58
                                                                                                                                                                                                                                                                                            Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP2004229667-A.
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                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR72987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR72987
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The invention relates to Lawsonia intracellularis HypC protein and a nucleotide sequence that encodes L. intracellularis HtrA, PonA, HypC, LysS, YCfW, ABCI, orfi and Omp100 protein. The invention also relates to an immunogenic composition or vaccine comprising an immunogenic amount of the proteins of the invention in combination with a pharmaceutical carrier. The composition is useful for diagnosing or preventing infections caused by L. intracellularis porcine proliferative enteropathy (PPE) in susceptible animals such as pigs. The present sequence is a primer used for sequencing pER392 Lawsonia intracellularis gene cluster B containing HtrA, PonA, HypC and Orfl genes.
                                               New isolated Lawsonia intracellularis HypC proteins useful for diagnosing or preventing infections caused by L. intracellularis in susceptible animals, such as pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Motilin receptor; gastrointestinal disease; gastric motility disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide in unique region in exon 1 of rabbit motilin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Score 13.2; DB 14;
                                                                                                                                                                Example 2; SEQ ID NO 50; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGGTACAGCAAGAAAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TGTTACAGGTAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF85459 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
WPI; 2005-457804/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Local Similarity

4 TGTTACAGGTAGAAAGC 21 regracaccaacaaaacc 19

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The invention relates to an antisense oligonucleotide or its active derivative selected from AEC46374-AEC46395, targeting human interleukin-CC derivative selected from AEC46374-AEC46395, targeting human interleukin-CC do (IL-10). Also included are a process of manufacturing the antisense oligonucleotide (or its active derivative, by adding consecutive congrising to nucleosides and linker stepwise or by cutting the Oligonucleotide out of nucleosides and linker stepwise or by cutting the Oligonucleotide in comprising a composition for treating cancer. The oligonucleotide is an antisense congosition for treating cancer. The oligonucleotide is an antisense coligonucleotide inhibiting the synthesis of proteins involved in the formation of metastases. The oligonucleotide is an antisense coligonucleotide inhibiting the production of transforming growth factor (TGP)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules (TAMS) and/or interleukins 10. The oligonucleotides are colimbitors (TIMPS) and/or interleukins 10. The oligonucleotides are useful for the preparation of a pharmaceutical composition for inhibiting the formation of metastases in cancer treatment. The oligonucleotides are useful for treating cancer, bronchogenic carcinoma, carcinoma, cellorectal carcinoma, cervical cancer, bronchogenic carcinoma, collorectal carcinoma, cervical cancer, epithelial carcinoma, collorectal carcinoma, eactinoma, usefullary adenocarcinoma, prostate cancer, gall bladder carcinoma, lung carcinoma, medullary carcinoma, papillary adenocarcinoma, prostate cancer, small collorect cancer, papillary carcinoma, vertal cancer, setting ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ewing's tumor, craniopharyngioma, ependymoma, medulloblastoma, hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma, neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas, Wilm's tumor and/or myeloma, multiple. The present sequence is an
                                                                                                                                          New antisense oligonucleotides inhibiting the synthesis of proteins involved in the formation of metastases such as transforming growth factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
              Stauder G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming growth factor beta; TGF-beta-3; antisense therapy; antisense oligonucleotide; ss; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 87.5%; Score 12.8; DB 14; Length 18; Similarity 87.5%; Pred. No. 2.2e+04; L4; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide targeting human TGF-beta-3 #304.
           Jachimczak P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotide targeting human TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
        Schlingensiepen K, Schlingensiepen R,
                                                                                                                                                                                                                                                                               Claim 4; Page 71; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멾
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TACAGGGAGAAATCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEC51906 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TACAGGTAGAAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
nes 14; Conservative
                                 Bischof A, Hafner M,
                                                                                       WPI; 2005-630685/64.
                                                                                                                                                                                                                               treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEC51906/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP85456-60 represent polynucleotide sequences from the unique region of exon 1 of a rabbit motilin receptor gene. The specification describes an unique sequence present in exon 1 of the motilin receptor, which is not present in human or Sphaeroides nephelus 7587 motilin receptor sequences. The unique nucleic acid sequence is useful for measuring the ability of a compound to affect motilin receptor activity. Motilin receptor polynucleotides and polypeptides are useful for treating castrointestinal diseases and disorders such as gastric motility disorders, gastroparesis, irritable bowel syndrome, and diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptides related to dog and rabbit motilin receptor polypeptide, comprising unique regions from dog and motilin receptor amino acid sequence, useful for identifying compounds for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming growth factor beta, TGF-beta-3; antisense therapy; antisense oligonucleotide; ss; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotide targeting human TGF-beta-3 #444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 59.1%; Score 13; DB 4; Length 22;
1 Similarity 100.0%; Pred. No. 1.8e+04;
13; Conservative 0; Mismatches 0; Indels
gastroparesis; irritable bowel syndrome; diarrhoea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 2 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEC52046 standard; DNA; 18 BP.
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                                                                                                                                                                                                                 25-OCT-2000; 2000WO-US029426
                                                                                                                                                                                                                                                                         99US-0162264P
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01-APR-2004; 2004US-0558135P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC.
                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-343479/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diarrhea in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  Mckee K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2005084712-A2.
                                                                                                     WO200132710-A1.
                                                                                                                                                                                                                                                                    29-OCT-1999;
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                                                                                                                                                              10-MAY-2001
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Query Match

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AEC52046;

AEC51766;

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The invention relates to an antisense oligonucleotide or its active derivative selected from AEC46374-AEC46395, targeting human interleukin-
10 (IL-10). Also included are a process of manufacturing the antisense oligonucleotide (or its active derivative, by adding consecutive oligonucleotide chain), a pharmaceutical composition comprising the antisense oligonucleotide chain), a pharmaceutical composition comprising composition for treating cancer. The oligonucleotide is an antisense composition for treating cancer. The oligonucleotide is an antisense coligonucleotide inhibiting the synthesis of proteins involved in the formation of metastases. The oligonucleotide is an antisense coligonucleotide inhibiting the production of transforming growth factor (TGP)-beta 1, TGF-beta 2, TGF-beta 3, cell-cell adhesion molecules coligonucleotide inhibitions interleukins 10. The oligonucleotides are coligonucleotide and coligonucleotides are inhibitors (TIMPS) and/or interleukins 10. The oligonucleotides are useful for the preparation of a pharmaceutical composition for inhibiting the formation of metastases in cancer treatment. The oligonucleotides are useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma, colon carcinoma, colorectal carcinoma, carcinoma, cancer, partical cancer, colorectal carcinoma, carcinoma, colon carcinoma, medullary carcinoma, neces, papillary adenocarcinoma, medullary carcinoma, lung carcinoma, medullary carcinoma, non-small cell connecting papillary accinoma, medullary carcinoma, papillary adenocarcinoma, prostate cancer, squamous call carcinoma, carcinoma, ectal carcinoma, papillary adenocarcinoma, papillary adenocarcinoma, papillary adenocarcinoma, papillary accinoma, papillary accinom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hemangioblastoma, medillabiastoma, melanoma, mesothelioma, neuroblastoma, neuroblastoma, neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas, Wilm's tumor and/or myeloma, multiple. The present sequence is an antisense oligonucleotide targeting human TGF-beta-3.
                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides inhibiting the synthesis of proteins involved in the formation of metastases such as transforming growth factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for
                                                                                                                                                                                                                                                                  Stauder G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ewing's tumor, craniopharyngioma, ependymoma, medulloblastoma,
                                                                                                                                                                                                                                                                Jachimczak P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 2 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Schlingensiepen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 70; 106pp; English.
                                                                                                                                                                                                                                                                                         Egger T;
                                                                                                                                                                                                               (ANTI-) ANTISENSE PHARMA GMBH
                                                                                           28-FEB-2005; 2005WO-EP002101.
                                                                                                                                       27-FEB-2004; 2004EP-00004478.
                                                                                                                                                                01-APR-2004; 2004US-0558135P
                                                                                                                                                                                                                                                                                    Bischof A, Hafner M,
                                                                                                                                                                                                                                                                                                                                     WPI; 2005-630685/64.
                                                                                                                                                                                                                                                             Schlingensiepen K,
WO2005084712-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating cancer.
                                              15-SEP-2005
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                                    Gaps
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58.2%; Score 12.8; DB 14; Length 18; 87.5%; Pred. No. 2.2e+04; ive 0; Mismatches 2; Indels (
                 11 Similarity 87.5%;
14; Conservative
Query Match
Best Local Similarity
                                  Matches
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17 TACAGGAGAGAATCC 2
                                                   RESULT 12
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22

7 TACAGGTAGAAAAGCC

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AEC51766 standard; DNA; 18 BP.

AEC51766/c ID AEC51 XX

The invention relates to an antisense oligonuclectide or its active derivative selected from AEC46374-AEC46395, targeting human interleukinC derivative selected from AEC46374-AEC46395, targeting human interleukinC 10 (IL-10). Also included are a process of manufacturing the antisense oligonuclectide chain), a paramaceutical composition comprising the product of interlectide chain), a paramaceutical composition comprising the antisense oligonuclectide chain), a paramaceutical composition comprising the antisense oligonuclectide inhibiting the synthesis of proteins involved in the cormation of metastases. The oligonuclectide is an antisense oligonuclectide inhibiting the production of transforming growth factor (TGP)-beta 1, TGP-beta 2, TGP-beta 3, cell-cell adhesion molecules
CC (TGMS) integrins, selectins, metalloproceases (WMPS), their tissue inhibitors (TIMPS) and/or interleukins 10. The oligonuclectides are cuseful for the preparation of a pharmaceutical composition for inhibiting the formation of metastases in cancer treatment. The oligonuclectides are useful for treating cancer, e.g. bile duct carcinoma, bladder carcinoma, cloracinoma, color carcinoma, sepitalial carcinoma, espatical cancer, papillary adenocarcinoma, papillary carcinoma, papillary carcinoma, papillary carcinoma, papillary adenocarcinoma, papillary carcinoma, papillary carcinoma, papillary denocarcinoma, papillary carcinoma, papillary denocarcinoma, papillary denocar, cancer, papicolar cancer, canc hemangioblastoma, medullablastoma, melanoma, mesothelioma, neuroblastoma, neuroblastoma, neurofibroma, pinealoma, retinoblastoma, sarcoma, seminoma, trachomas, Wilm's tumor and/or myeloma, multiple. The present sequence is an New antisense oligonucleotides inhibiting the synthesis of proteins involved in the formation of metastases such as transforming growth factor-beta 1 (TGF-beta 1), TGF-beta 2 and TGF-beta 3, useful for Stander G; Transforming growth factor beta; TGF-beta-3; antisense therapy; antisense oligonucleotide; ss; cancer; cytostatic. Antisense oligonucleotide targeting human TGF-beta-3 #164. Schlingensiepen K, Schlingensiepen R, Jachimczak P, Bischof A, Hafner M, Egger T; antisense oligonucleotide targeting human TGF-beta-3. Claim 4; Page 70; 106pp; English. (ANTI-) ANTISENSE PHARMA GMBH 28-FEB-2005; 2005WO-EP002101. 27-FEB-2004; 2004EP-00004478. 01-APR-2004; 2004US-0558135P. 17-NOV-2005 (first entry) WPI; 2005-630685/64. treating cancer. WO2005084712-A2. Homo sapiens. 15-SEP-2005,

DB 14; Length 18; Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other; Pred. No. 2.2e+04; Score 12.8; 58.2%; 87.5%; Best Local Similarity Query Match

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The invention relates to a human prostate cancer predisposing gene coding for an HPC2 polypeptide. The DNA and protein sequences are useful as diagnostic reagents for identifying a mutent HPC2 nucleotide sequence in a suspected mutant HPC2 allele by comparing the sequence of the suspected mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also useful for detecting an alteration in HPC2, where the alteration is associated with cancer in a human. The method involves analysing an HPC2 gene or an HPC2 gene expression product from a tissue of the human. The HPC2 gene is useful as a marker for prostate cancer and can be used in gene therapy techniques to suppress neoplastic growth of recipient cells which carry the mutant HPC2 allele. The sequences represent primers used in the methods of the invention, cDNA encoding human and mouse HPC2 and
                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker for prostate cancer, is useful in gene therapy techniques to restore HPC2 normal levels by which neoplastic growth is suppressed in recipient cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe; HMG box; human; bovine; sex; animal; birth; ss.
      gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla; sequencing primer; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.2%; Score 12.8; DB 6; Length 19; 87.5%; Pred. No. 2.2e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                               Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding HPC2 paralogues and orthologues
                                                                                                                                                                                                                                                                                                                        Tavtigian SV, Teng DHF, Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 74; 239pp; English.
                                                                                                                                                                                                                                                               (MYRI-) MYRIAD GENETICS INC.
(HOSP-) HOSPITAL FOR SICK CHILDREN.
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Best Local Similarity 87.5%;
Conservative
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ID AAT33010 standard; DNA; 20
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                                                                                                      WO200185911-A2
                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human version of the gene is found on chromosome 17p. Some alleles cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide done therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a primer used in the isolation of the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;
    Gaps
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                                                                                                                                                                                                                                                                                                                                   Human, mouse, prostate cancer predisposing gene, HPC2;
human chromosome 17p; gene therapy; peptide therapy; drug design;
PCR primer; sequencing primer; ss.
                                                                                                                                                                                                                                                                                              Human HPC2 cDNA exon 18 mutation screening primer SBQ ID NO: 157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 58.2%; Score 12.8; DB 3; Length 19; ll Similarity 87.5%; Pred. No. 2.2e+04; 14; Conservative 0; Mismatches 2; Indels
    Indels
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  Mismatches
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                                     7 TACAGGTAGAAAAGCC
                                                                            TACAGGGAGAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
14; Conservative
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Matches
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AAS99071/c
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(KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU,
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WPI; 1996-336575/34.

Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex of unborn animals.

Example 2; Page 6; 21pp; Japanese.

The primers AAT33009-10 were used to amplify a fragment of the gene encoding a mouse SRY-related protein (AAT33007). This primer corresp. to bases 7156-7175 of the mouse gene. The amplified fragment was used to screen a mouse genomic library. The screen isolated 4 EcoRI fragments of 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed a human SRY HMG box sequence between bases 7154-7393. Similarity with the human SRY HMG box sequence resulted in primers being generated to amplify the human SRY HMG box sequence for use as a probe to isolate the bovine SRY-related gene (AAT33008). The mouse and bovine genes are useful for determining the sex of an animal prior to birth 

Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Gaps ö Query Match 58.2%; Score 12.8; DB 2; Length 20; Best Local Similarity 87.5%; Pred. No. 2.2e+04; Matches 14; Conservative 0; Mismatches 2; Indels

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20 TGCAGGTGGAAAAGCC 5

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Search completed: June 8, 2006, 21:51:02 Job time : 294 secs

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7 TACAGGTAGAAAAGCC 22

Recombina

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Database

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BD014939 21 bp DNA linear PAT 27-AUG-2002 Lawsonia intracellularis protein and methods and materials relating thereto.
BD014939 GI:22555746
BD014939-1 GI:22555746
Lawsonia intracellularis
        AR234243 Sequence
AR291044 Sequence
AR481045 Sequence
AR481107 Sequence
AR271107 Sequence
AR271107 Sequence
AR271107 Sequence
AR271107 Sequence
AR181897 Sequence
AR18897 Sequence
AR18897 Sequence
AR18897 Sequence
AR137295 Sequence
AR571186 Sequence
CS102002 Sequence
CS102139 Sequence
AR3496 Synthetic
AR162418 Sequence
AR3496 Synthetic
AR405006 Sequence
                                                                                                                                                                                                                                                                                                                       PAT 12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 20)

Griffals, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
Chlamydia pnewmoniae polymucleotides and uses thereof
Patent: US 6559294-A 5333 06-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.1%; Score 15.2; DB 2; Length 20; 85.0%; Pred. No. 2.7e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                     20 bp DNI
Sequence 5333 from patent US 6559294.
AR314796
                                                                                                                                                                                                                                                                        ALIGNMENTS
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/organism="unknown"
/mol_type="genomic DNA"
        AR234243
AR293044
AR293044
AR29864
AR271107
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AR162418
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AX405006
AX405010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATGTTACAGGTAGAAAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTGTTCCAGATAGAAAG 1
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Best Local Similarity 85.0
Matches 17; Conservative
Unknown
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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AUTHORS
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AK13464 Sequence
BD231604 Chromosom
AR63169 Sequence
AR65265 Sequence
CQ875125 Sequence
CQ875125 Sequence
CC8009920 Sequence
CS006043 Sequence
CS06074 Sequence
CS06075 Sequence
AR138875 Sequence
                                                          8, 2006, 21:46:16; Search time 1977 Seconds (without alignments) 711.605 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR314796 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                    1227620
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                6366136 segs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
                                         nucleic search, using sw model
                                                                                                                   gcatgttacaggtagaaaagcc 22
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AR374844
AR374844
BD231604
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AR652656
AX4000934
CC0976341
CS000920
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Homo sapiens
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                                                          Rosi,I.L.
Lawsonia intracellularis protein and methods and materials relating
                                                                                                   Patent: JP 2001169787-A 43 26-JUN-2001;

PFIZER PRODUCTS INC

S Lawsonia intracellularis

BN JP 2001169787-A/43

PD 26-JUN-2001

PP 20-CT-2000 JP 2000320736

PP 22-OCT-1999 US 60/160922

PI IBURETTO LEE ROSI

PP C12N15/09, A61K38/00, A61K38/106, A61K48/00, A61P31/04, C07K14/205,
                                                                                                                                                                                                                                                                                        C12P21/08, (C12P21/02,C12R1:19),C12N15/00,A61K37/02,C12N5/00 CC Lawsonia intracellularis protein and methods and materials CC
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              Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Lawsonia.
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    /organism='Lawsonia intracellularis'.

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Patent: US 6605696-A 50 12-AUG-2003;
Pfizer, Inc. and Pfizer Products, Inc.; New York, NY
Location/Qualifiers
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/organism="Lawsonia intracellularis"
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Sequence 50 from patent US 6605696.
AR374844.1 GI:40077832

    .21
    /organism="unknown"
    /mol_type="genomic DNA"

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/db_xref="taxon:29546"
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Unclassified.
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PN JP 2001
PP 20-0TN-
PR 22-OCT-
PR 22-OCT-
PC C12N15/
PC C12N15/
PC C12P11/02,
PC C12P21/02,
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Matches 15; Conserv
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AR374844
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PAT 30-MAY-2001
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BD231604
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G01N33/57,
G01N37/00,C12N15/00,A61K37/02,C12N5/00
Chromosome 17q-linked prostate cancer susceptibility gene FH Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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JP 200252965-A/156
10-58P-2002
5005-NOV-1999 US 60/107468
SEAN V TAVTIGIAN, DAVID H F TENG, JACQUES SIMARD, JOHANNA M PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1 (Dases 1 to 19)

Tartigian, S.V., Teng, D.H.F., Simard, J. and Rommens, J.M.
Chromosome 17q-11nked prostate cancer susceptibility gene
Patent: JP 2002529065-A 156 10-SEP-2002;
MYRIAD GENETICS INC, THE HOSPITAL FOR SICK CHILDREN
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/mol_type="unassigned DNA"
/db_xref="taxon:29546"
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    DNA
                                                                                                                                                                                                                                                                       materials
Patent: EP 1094070-A 50 25-APR-2001;
Pfizer Products Inc. (US)
AX139516 21 bp
Sequence 50 from Patent EP1094070.
AX139516

    .19
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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PAT 14-JUN-2002
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                                                                                                                                                                                                Choo, Y. and Isalan, M. Method for the preparation of selectively randomised nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cobleigh, M.A., Shak, S., Baker, J.B. and Cronin, M.T.
Gene expression markers for breast cancer prognosis
Patent: WO 2004065583-A 191 05-AUG-2004,
Genomic Health, Inc. (US); Rush University Medical Center (US)
Location/Qualifiers
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61.1%; Pred. No. 4.8e+05;
iive 5; Mismatches 2;
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/mol_type="unassigned DNA"
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Sequence 80 from Patent WO2004111603.
CQ975123. GI:57999022
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synthetic construct
other sequences; artificial sequences.
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other sequences; artificial sequences.
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Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Sequence 25 from Patent W00222634.
AX405008
AX405008.1 GI:21438223
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19 TSYKCGAGKYAGAAAAGC 2
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CQ876341/c
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                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 19)

Tavtigian, S.V., Teng, D.H.-F., Simard, J., Rommens, J.M., Cannon Albright, L.A. and Neuhausen, S.L.
Chromosome 1.P-linked prostate cancer susceptibility gene Patent: US 6844189-A 157 18-JAN-2005;
Myriad Genetics, Inc., University of Utah Research Foundation and Hospital for Sick Children; Salt Lake City, UT
                                                                  Gaps
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Monia, B.P. and Freier, S.M.
Antisense modulation of transforming growth factor-beta 3
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58.2%; Score 12.8; DB 2;
Best Local Similarity 87.5%; Pred. No. 4.8e+05;
Matches 14; Conservative 0; Mismatches 2;
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Patent: US 6884787-A 75 26-APR-2005;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
Location/Qualifiers
                                                                                                                                                                                                               DNA
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Sequence 157 from patent US 6844189.
AR631469.1 GI:59771253
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/organism="unknown"
/mol_type="genomic DNA"
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Unclassified.
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AR631469/c
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AR652656/c
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PAT 13-APR-2005

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Modulation of eifte expression
Patent: WO 2005038628-A 116 31-MAR-2005,
Isis Pharmaceuticals, Inc. (US); Eli Lilly and Company (US)
Location/Qualifiers
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Modulation of eif4e expression
Nocologo 205028628-A 201 31-MAR-2005;
Isis Pharmaceuticals, Inc. (US); Eli Lilly and Company (US)
Location/Qualifiers
                                                                                                                                              /mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target
sequence/siNA antisense region"
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                                                                                                                                                                                                                                                                                                                 57.3%; Score 12.6; DB 2; 78.9%; Pred. No. 6.1e+05; tive 0; Mismatches 4;
     Patent: WO 2005007855-A 152 27-JAN-2005;
Sirna Therapeutics, Inc. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                     /organism="synthetic construct"
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Sequence 201 from Patent WO2005028628.
CS060728
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Best Local Similarity 78.9
Matches 15; Conservative
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RNA interference mediated inhibition of B7-H1 gene expression using short interfering Nucleic Acid (siNA)

Batent: WO 2005,007855-A 66 27-JAN-2005;

Sirna Therapeutics, Inc. (US)

Location/Qualifiers
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                                                                                                      Baker, J.B., Miller, K.D., Shak, S., Sledge, G.W. and Soule, S.U. Gene expression markers for predicting response to chemotherapy Patent: WO 2004111603-A 80 23-DEC-2004; Genomic Health, Inc. (US)
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87.5%; Pred. No. 4.7e+05;
iive 0; Mismatches 2;

    .21
    forganism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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CS009834
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                                                                                                                                                                                                                                                                                                                                                                     /note="reverse primer"
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Matches 14; Conservative
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CS009834
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Modulation of sifte expression
Patent: WO 2005028628-A 230 31-MAR-2005;
Isis Pharmaceuticals, Inc. (US); Eli Lilly and Company (US)
Location/Qualifiers
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                                                                                      Query Match 57.3%; Score 12.6; DB 2; Length 20; Best Local Similarity 78.9%; Pred. No. 6.1e+05; Matches 15; Conservative 0; Mismatches 4; Indels
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synthetic construct
other sequences; artificial sequences.
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||| || || || || || || || || || || 2
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Search completed: June 8, 2006, 22:24:02 Job time: 1978 secs

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Title: Perfect score:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 22)

2 (bases 1 to 22)

Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Relly,M., Rose,M., Sci, Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stoke,M., Stok
AZ799032 ZM0056K07
AJ596498 Arabidops
AZ43039 1M012B12
AZ483039 1M012B121
AZ786362 ZM0031N16
CL66834 PR101586
AZ796022 1M0160J26
CZ443105 IBB8P10.f
CL687844 PR10147d
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AZ817291 ZM008912
AZ817291 ZM008812
AZ817291 ZM0084N15
AZ76032 IM0053N15
AZ76232 AZ76039
AZ612157 IM043ĒL21
AZ817291 ZM008812
AZ348213 IM0084N15
AZ76032 ZM059D13
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1M0536B16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0536B16 F, genomic survey sequence.
AZ659094
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Plate: 0536 row: E column: 16
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/strain="C57BL/6J"
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AZ4830498

AZ483078

AZ483078

AZ786322

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CL687844

AZ312947

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CT01796099

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DU835192
AZ357874
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Mus musculus (house mouse)
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AZ45226 1M052H06
CL681335 PF10130d
AZ651001 1M0521003
AZ775974 2M0009H14
AZ990555 2M0274N14
DUB30438 KBF15006K2
AZ649514 1M0519A09
AZ649514 1M0519A09
AZ75273 2M000F04
AZ75273 2M000F04
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AZ882923 2M0105B09
AZ88233 2M0105B09
AZ88233 2M0105B09
AZ828233 2M0105B09
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AZ625409 1M0464C20
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                                                                                          8, 2006, 21:51:16 ; Search time 2259 Seconds (without alignments) 544.588 Million cell updates/sec
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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                  nucleic search, using sw model
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Tector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut cond-repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shoared in the polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kD). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. bruce! sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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AL495341.1 GI:11871728
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hii Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.7%; Score 13.8; DB 11; Length 22; 88.2%; Pred. No. 7.8e+04; ive 0; Mismatches 2; Indels (
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Best Local Similarity 88.2
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/db\_xref="taxon:5691" /clone="359f10"

ORIGIN

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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut cand-repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose ger
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114 | gb | AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurcognathi; Murcidea; Muridae; Musinae; Mus.

1 (bases 1 to 20)
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1 (bases 3 to 20)
1 (bases 3 to 20)
1 (bases 4 to 20)
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Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                 Gaps
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     50.9%; Score 11.2; DB 14; Length 20; 81.2%; Pred. No. 1.4e+06; ive 0; Mismatches 3; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0252 row: H column: 06
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/clone="UUGC1M0252H06"
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                                                                                                                                                                                                                                      6 TTACAGGTAGAAAGC
Query Match
Best Local Similarity 81.2°
Matches 13; Conservative
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Fax: 801 585 7177
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LOCUS DEFINITION

RESULT 4 CL681335

ò 셤 SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

PUBMED COMMENT

FEATURES

ORIGIN

JOURNAL

ACCESSION VERSION

KEYWORDS

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 gib Jh22072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
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                       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Dunal,B., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Mennen,B., PederBen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Pred. No. 2.2e+06;
0; Mismatches 2; Indels
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.
Plate: 0521 row: 0 column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends

    .22
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/clone="UUGC1M0521023"
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High quality sequence stop: 22.
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AZ775974
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1M0521023F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0521023 F, genomic survey sequence.
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires; Rodentia,
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/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
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Neodiplogasteridae; Pristionchus.
1 (bases 1 to 20)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                               Gaps
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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                                       50.0%; Score 11; DB 11; Length 20; 100.0%; Pred. No. 1.7e+06;
                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenanustr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
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Pred. No. 2.2e+06;
0; Mismatches 2;
                                                                                          0; Mismatches
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/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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AZ651001.1 GI:11786054
GSS.
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Pristionchus pacificus
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85.7%;
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Best Local Similarity 85.7*
Matches 12, Conservative
                                                               Best Local Similarity 100.
Matches 11; Conservative
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ACCESSION VERSION KEYWORDS SOURCE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gil-f4732114 [gb]-RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent R. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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DU830438
DU8310438.1 GI:83867034
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/clone lib="Mouse 10kb plasmid UUGCZM library"
/note="Vector: PWDATUY; Purified genomic DNA from M.
musculus C578L/67 (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Musinae; Mus. 1 (2022)
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Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC2M0274N14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnarea/). The DNA
was blut. For it is at constant velocity. The sheared DNA
was blut end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose general from a derivative
of pWD42 (gil |4732114|gb|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
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48.2%; Score 10.6; DB 11; Length 20;
Best Local Similarity 76.5%; Pred. No. 2.7e+06;
Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: H column: 14
Seg primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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/clone="UUGC2M0009H14"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AZ990555/c DEFINITION

RESULT 7

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Pax: 801 585 7177
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Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Brastyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Grantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicacea; Brassica.

E 1 (bases 1 to 22)

S Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Saulal (KBrS) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 21)
S Dum, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,R., Pedersen,T., Rellly,M., Rose,M., Stokes,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Dasmid inserts
Unpublished (2000)
L Context: Robert B. Weiss
University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                     Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="KBrS006K24"
/lab host="B. coli DH10B"
/clone lib="KBrS Brassica rapa Sau3AI BAC library"
/clone lib="Wetcr: gruGIBAC1; Site 1: Sau3A1; Brassica rapa
spp pekinensis var. Chiifu BAC library (KBrS BAC) is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                            National Institute of Agricultural Biotechnology 225 Seodum-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Pax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="pekinensis"
/db_xref="taxon:51351"
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Tel: 801 585 5606
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gi|473214]qb|A123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0519 row: A column: 09
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plaemid ends
                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
                                                                                                                                                                                  High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="UUGC1M0519A09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|473214 gip|A123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU008116 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe late spc02889, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clome llb="Mouse 10kb plasmid UGGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.

1 (bases 1 to 20)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
         Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 45.5%; Score 10; DB 11; Length 19; Best Local Similarity 72.2%; Pred. No. 5.2e+06; Matches 13; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                              Std Error: 0.00
                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0
Plate: 0007 row: P column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0007F04"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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                                                          plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU008116
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                                                                                                                                                                     info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ775273 16-FEB-200 2M0007F04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0007F04 R, genomic survey sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="26 somite embryos, adult livers, shield
stage embryos"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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0
                                                                                                                                                                                                                                                     Trace Considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: T3 ET from Amersham
High quality sequence stop: 1
POLYA-NO.
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Pred. No. 5.2e+06;
0; Mismatches 5; Indels
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/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE:3717229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Best Local Similarity 72.2°
Matches 13; Conservative
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RESULT 11 AZ775273/c DEFINITION

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ORIGIN

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KEYWORDS

REFERENCE AUTHORS

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/mol_type="genomic DNA"
/strain="C57BL/6J"
                  clone="UUGC1M0391M24"
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AZ828233.1 GI:12998141
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                                                                                                                                                                                 1. .20
/organism="Schizosaccharomyces pombe"
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc02889"
/sex="h minus"
/clone lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: Ml3mpl9; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Ml3mpl9 DNA and the direction of DNA
into the Smal site of Ml3mpl9 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nire.go.jp)"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
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1M0391M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0391M24 F, genomic survey sequence.
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1 (Dases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Blaim, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Waiss, R.
pombe
Unpublished (1998)
Contact: Mitsucki Morimyo
Genome Research Group
Genome Institute of Radiological Sciences
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Bmail: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 45.5%; Score 10; DB 1; Length 20; l Similarity 72.2%; Pred. No. 5.3e+06; 13; Conservative 0; Mismatches 5; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: M column: 24
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@qenet
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Matches 13; Conserva
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KEYWORDS
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                                                    COMMENT
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalot (gilfa732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0105B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0105B09 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Niederhausern, A. and Wright, D., Weiss, R.
Unpublished (2000)
Contact: Robert B.
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 5.3e+06;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                              /lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Monuse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chamically complementary to the insert adaptors and
purified. The sheared adaptored mouse DNA was annealed to
chamically constant and transformed into
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E 1 (bases 1 to 21)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Grome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Context: Robert B. Weiss
University of Utah
Genome Center
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2M0105B09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0105B09 F, genomic survey sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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                              UUGC2M0105B09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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AZ828233.1 GI:12998141
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AZ828233/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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COMMENT
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gilf4732114 [gpl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                             /db_xref="taxon:10090"
/clone="UUGC2M0105B09"
strain="C57BL/6J"
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Gaps .. Query Match 45.5%; Score 10; DB 11; Length 21; Best Local Similarity 100.0%; Pred. No. 5.3e+06; Matches 10; Conservative 0; Mismatches 0; Indels

ö

Search completed: June 8, 2006, 23:01:53 Job time : 2264 secs

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"GenCore version 5.1.9

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 22:10:54 ; Search time 100 Seconds

(without alignments)

411.644 Million cell updates/sec
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(without alignme 411.644 Million Title: US-09-743-825-7 Senfect score: 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 576012

Minimum DB seq length: 0 Maximum DB seq length: 22 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Issued Patents NA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			df			SUMMARIES	
Result No.	ult No.	Score	Query Match	Query Match Length DB	DB	ID	Description
ט	-	15.2	69.1	20	6	US-09-198-452A-5333	Sequence 5333, Ap
	7	13.2	60.0	21	m	US-09-689-065B-50	
	m	13.2	60.0	21	4	US-10-210-296A-50	20,
O	4	12.8	58.2	19	m	US-09-564-805-157	157,
υ	Ŋ	12.8	58.2	19	m	US-09-434-382-157	Sequence 157, App
O	9	12.8	58.2	20	e	US-09-906-158-75	75, A
	7	12.2	55.5	18	ო	US-08-840-316-53	23,
	æ	12.2	55.5	18	ო	US-08-809-523-53	53,
	σ	12.2	55.5	18	٣	US-08-471-971-53	53,
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Sequence 29, Appl	4	Sequence 702, App	Sequence 703, App	Sequence 704, App	Sequence 705, App	Sequence 1534, Ap	Sequence 79, Appl		Sequence 702, App	•	Sequence 704, App	Sequence 705, App	Sequence 79, Appl		•	Sequence 7261, Ap	Sequence 27, Appl	7. A	34,	Sequence 38, Appl	Sequence 6684, Ap
Sedu	Sedu	Sedu	Sedu	Sequ	Sedu	Sedu	Sedu	Sequ	Secto	Sequ	Sequ	Sequ	Sedu	Sequ	Sequ	Sedu	Sedu	Sedu	Sedu	Sequ	Sedu
US-09-648-520B-29	US-09-422-978-4544	US-08-985-162-702	US-08-985-162-703	US-08-985-162-704	US-08-985-162-705	US-08-584-040-1534	US-09-371-772B-79	US-09-371-772B-4284	US-09-401-063-702	US-09-401-063-703	US-09-401-063-704	US-09-401-063-705	US-09-685-664B-79	US-10-138-674B-79	US-10-138-674B-4284	US-10-138-674B-7261	US-08-981-988A-27	US-09-531-000-7	US-09-531-000-34	US-09-531-000-38	US-09-422-978-6684
19 3	19 3	17 3	17 3	17 3	17 3	17 3	17 3	17 3	17 3	17 3	17 3	17 3	17 3	17 5	17 5	17 5	18 3	19 3	19 3	19 3	19 3
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C 24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT 1
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US-09-198-452A-5333/c
Sequence 533, Application US/09198452A
Fatent No. 6559294
Fatent No. 659294
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Fatent No. 65929
Fatent No. 659299
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RESULT 2
US-09-689-065B-50
Squence 50, Application US/09689065B
Squence 100 Experiment 100

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US-09-564-805-157
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US-10-210-296A-50

Sequence 50, Application US/10210296A

Patent No. 698214

GENERAL INFORMATION:
TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED METHODS AND TITLE OF INVENTION: MATERIALS

FILE REFERENCE: 3153.00355/PC10589B

CURRENT APPLICATION NUMBER: US/10/210,296A

CURRENT FILING DATE: 2000-00-01

PRIOR APPLICATION NUMBER: US 60/160,922

PRIOR FILING DATE: 1999-110-2

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 110

SOFTWARE: Patentin version 3.2

LENGTH: 21

LENGTH: 21
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APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: 1999-11-05
FRIOR FILING DATE: 1999-11-05
FRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 157
LENGTH: 19
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                                                                                                           Length 21;
                                                                                                                                                    3; Indels
                                                                                                    Query Match
60.0%; Score 13.2; DB 3;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 157, Application US/09564805
Patent No. 6333403
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-09-689-0658-50
                                                                                                                                                                                                                      2 TGGTACAGCAAGAAAGC 19
                                                                                                                                                                                      4 TGTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 TGTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 regracaccaacaaaacc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-564-805-157/c
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Sequence 75, Application US/09906158
Fatent No. 6884787
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
APPLICANT: Breat P. Monia
FILE REFERENCE: RTS-0257
CURRENT APPLICATION VUMBER: US/09/906,158
CURRENT FILING DATE: 2001-07-14
NUMBER OF SEQ ID NOS: 168
ILENGTH: 20
                                                                                                                                                                                                                                                                                       APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene
FILE REFERENCE: HPC2 Gene
CURRENT APPLICATION NUMBER: US/09/434,382
CURRENT FILING DATE: 1999-11-06
MUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 157
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                  58.2%; Score 12.8; DB 3; Length 19; 87.5%; Pred. No. 7.1e+03; live 0; Mismatches 2; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.2%; Score 12.8; DB 3;
87.5%; Pred. No. 7.1e+03;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide US-09-906-158-75
                                                                                                                                                                                                                                Sequence 157, Application US/09434382; Patent No. 6844189; GENERAL INFORMATION:
                                                                                                 3 ATGTTACAGGTAGAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ATGTTACAGGTAGAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TACAGGTAGAAAAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 ATGTCACAGGCAGAAA 4
                                                                                                                                        19 ATGTCACAGGCAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 87.5
Matches 14; Conservative
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-434-382-157
Query Match
Best Local Similarity
                                                                                                                                                                                                                     US-09-434-382-157/c
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US-09-906-158-75/c
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US-08-471-971-53
; Sequence 53, Application US/08471971
; Sequence 53, Application US/08471971
; Patent No. 6287759
; GENERAL INFORMATION:
; APPLICANT: TRAREV, Sergei. A., Emerson,
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Nee in Diagnostic Methods And Vaccines
; TUBER OF SEQUENCES:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; STREET: 345 PARK AVENUE
; STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,971
FILING DATE: 06-UN-1995
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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Best Local Similarity
Matches 14; Conserva
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Batent No. 6207416

GENERAL INPORMATION:
APPLICANT: Tearev, Sergei. A., Emerson,
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE

COUNTRY: USA

STATE: NEW YORK

STATE: NEW YORK

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                      Sequence 53, Application US/08840116
Patent No. 6054567
GENERAL INFORMATION:
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Temerson, Sergei. A., and Robinson, Robin A.
TILLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                         ADDRESSE; MORGAN & FILLELL
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,316
FLILNG DATE: 1-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
FILING DATE: FLOPPY DISK
CLASSIFICATION: 424
ATTOREY/AGENT INFORMATION:
MAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION OF 53:
ENGURNE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GTTACAGGTAGAAAGC 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 82.4
Matches 14; Conservative
                US-08-840-316-53
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US-08-809-523-53
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Gaps
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MEDIUM TYPE: FLOATE LIBAR
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY-1997
RIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1994
FILING DATE: 03-OCT-1995
FILING DATE: 03-OCT-1994
FILING DATE: 03-OCT-1995
FILING DATE: 03-OC
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ZUP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,246
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 53, Application US/08470246
Patent No. 6696242
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                  5 GTTACAGGTAGAAAAGC 21
                                                                                                             2 GTTACAGCCAGAAACC 18
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Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TSARCY, SETGE
APPLICANT: SUZANDE U. P
TITLE OF INVENTION: RECO
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FIL
                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer_bind
                              Best Local Similarity
Matches 14; Conserv
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                    Query Match
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Pred. No. 1.4e+04;
0; Mismatches 3; Indels
                                         FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION NOMBER: US/US/VICE
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNDBER: 08/840,316
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
ERGURACE CHARACTERISTICS:
LENGTH: 18 DASS DAITE:
LENGTH: 18 DASS DAITE:
PRIOR APPLICATION DATA:
                                                                                                                                                                      TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               5 GTTACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                           2 GTTACAGCCAGAAACC 18
                                                                                                                                                                                                                                                                                                                Query Match 55.5%;
Best Local Similarity 82.4%;
Matches 14; Conservative (
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                      linear
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US-08-471-971-53
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US-09-402-776-53
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US-09-422-978-4779

Sequence 4779, Application US/09422978

Patent No. 653751

APPLICANT: Cohen, Daniel

APPLICANT: Chumakov, Ilva

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

PILE REFERENCE: GENEST.020CP1

CURRENT APPLICATION NUMBER: US/09/422, 978

CURRENT APLICATION NUMBER: US/09/422, 978

CURRENT PILING DATE: 1999-04-21

EARLIER PILING DATE: 1999-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4779
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                                               Gaps
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; OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-09-422-978-4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sergei. A., Emerson,
U., Purcell, Robert H.
Recombinant Proteins Of
A Pakistani Strain Of Hepatitis E And Their
Bes In Diagnostic Methods And Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
55.5%; Score 12.2; DB 3; Length 18; 82.4%; Pred. No. 1.4e+04; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.2; DB 3;
Pred. No. 1.4e+04;
0; Mismatches 3;
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LENGTH: 18 base pairs
                                                                                             ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-316-765-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-724-475-53
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APPLICANT: Tarrey, Sergei. A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE PORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA: 08/316,765
APPLICATION NUMBER: 03-OCT-1994
CLASSIFICATION DATA:
PRILING DATE: 03-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: USO7/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/POCKET NUMBER: 30,459
TELECOMMULICATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-0CT-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
INFORMATION FOR SED ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TERRORALION FOR SED ID NO: 53:
CENGTH: 18 base pairs
TERRORALION FOR SED ID NO: 53:
TERRORALION FOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 53, Application US/08316765
Patent No. 6706873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-470-246-53
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US-08-316-765-53
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Tsarev, Sergei. A., Emerson,
Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
A Pakistani Strain Of Hepatitis B And Their
Use In Diagnostic Methods And Vaccines
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    Length 18;
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                                                IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,475
FILING DATE: 28-No. 6787145-2000
RIOM APPLICATION DATA:
APPLICATION NUMBER: US/89,523
FILING DATE: 03-OCT-1994
APPLICATION NUMBER: US/89,16,765
FILING DATE: 03-OCT-1994
APPLICATION NUMBER: US/89,16,765
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BOTA
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 36,459
Score 12.2; DB 3;
Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSER: MORGAN & PINNEGAN, L.L.P. STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: USW YORK COUNTRY: USA
                                           0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                US-09-724-475-53
; Sequence 53, Application US/09724475
Patent No. 6787145
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                            5 GTTACAGGTAGAAAGC 21
                                                                                                                                      2 GTTACAGCCAGAAACC 18
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Query Match
Best Local Similarity 82.4%;
Matches 14; Conservative
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COMPUTER READABLE FORM:
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Gaps
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                                                                                                                                                                      5 GTTACAGGTAGAAAGC 21
                                                                                                                                                       Query Match
Best Local Similarity 82.4<sup>5</sup>
Matches 14, Conservative
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Search completed: June 8, 2006, 22:48:58 Job time : 101 secs

2 GTTACAGCCAGAAACC 18

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us-09-743-825-7.rnpbm

Fri Jun

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Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
                                                                                                                                                                                              June 8, 2006, 22:49:19; Search time 857 Seconds (without alignments) 315.435 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18892170 seqs, 6143817638 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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22
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	5333 Sequence 5333, Ap		A-163654 Sequence 163654,		-920023 Sequence 920023,			-935948 Sequence 935948,	A-353174 Sequence 353174,	4-805859 Sequence 805859,	A-353175 Sequence 353175,	Sequence			A-361013 Sequence 361013,	-29724 Sequence 29724, A	Sequence
SUMMARIES	US-10-289-762-5333	US-10-310-914A-1053240	US-10-310-914A-163654	US-10-310-914A-344929	US-11-083-784-920023	US-11-083-784-935948	US-11-101-244-920023	US-11-101-244-935948	US-10-310-914A-353174	US-10-310-914A-805859	US-10-310-914A-353175	US-10-310-914A-117024	US-10-310-914A-464518	US-10-310-914A-574946	US-10-310-914A-361013	US-11-083-784-29724	US-11-083-784-1359984
gth DB	20 7	22 11	20 11	22 11	19 14	19 14	19 15	19 15	21 11	21 11	22 11	19 11	22 11	22 11	19 11	19 14	19 14
% Query Match Length DB	69.1	4.99	65.5	64.5	62.7	62.7	62.7	62.7	62.7	62.7	62.7	6.09	6.09	6.09	0.09	0.09	0.09
Score	15.2	14.6	14.4	14.2	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.4	13.4	13.4	13.2	13.2	13.2
Result No.	ני	8	m	4	n N	9	c 7	80	6	c 10	11	12	13	c 14	c 15	16	17

RESULT 2 US-10-310-914A-1053240

Sequence 105240, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06

18	13.2	60.0	19	15	US-11-101-244-29724	Sequence	29724, A	
70	•	0.0	, c		US-II-IUI-Z44-I3559984	sednence	1359984,	
21	13.2	: 0	2 2	1 6	US-10-310-314M-223666 US-10-210-246-50	Seguence	50 Annl	
22		60.09	21		US-10-449-462-50	Segmence	0. Appl	
23		0	21		US-10-449-648-50		50. Ann	
C 24		60.09	22	::	US-10-310-914A-248351	Semence	248351	
25		60.0	22	11	US-10-310-914A-566298		566298	
26	12.8	58.2	18	11	US-10-310-914A-221112	Sequence	221112.	
		58.2	13	_ m	US-09-988-626-157	Sequence 1	57. App	
		58.2	10		US-09-988-687-157	Semience	57 400	
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36		58.2	19	4	US-11-083-784-683977		683977,	
37		58.2	19	14	US-11-083-784-948986		948986.	
38		58.2	19	4	US-11-083-784-949038		949038	
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42		58.2	19	14	US-11-083-784-1519908	Seguence	1519908,	
c 43		<u>.</u>	19	12	US-11-101-244-147360	Seguence	147360,	
44		'n.	19	15	-11-10	Segmence	614693	
C 45		58.2	19	12	4	Semience	676530	
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					ALIGNMENTS			
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US-10-2	US-10-289-762-5333/c	333/c						
; Seque	Sequence 5333, Application US/10289762	Applic	ation U	3/1	0289762			
. Publi	Publication No. US20040006218A1	. US200	4000621	841				
GRNED	GENERAL INFORMATION.	ANT TON.						
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STILL !		INVENTION:	thereo	E H	thereof and uses thereof, in particular	_	e diagnosis,	, preve
STITLE !	A OF INVENTION:	SNITTON	and tr	eati	ment of intection			
; FILE	FILE REFERENCE: 9710-003-999	E: 9710	-003-99					
CURR	CURRENT APPLICATION NUMBER:	CATION	NUMBER:		US/10/289.762			
CURR	CURRENT FILING DATE:	WG DATE:	2003-03-27		27			
NUMB	ER OF SEC	SON GI C						
L CRC .	SEC IN NO 5333	}						
7		•						
	LENGTH: 20							
; TYP	TYPE: DNA							
ORG		Chlamydia nneumonia	CHILAGO	ni a	4			
US-10-2	- 1	5333	Dillion of	1	)			
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Ouerv	Match		69.1		. 7	Length 20.		
Beat	Best Local Sim	Similarity	. 40			2		
Matches	es 17:	Conservative	42		. co+ac.	ċ		
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US-11-083-784-935948

i Sequence 935948, Application US/11083784

j Sequence 935948, Application US/11083784

j Publication No. US/0050245475A1

j GENERAL INFORMATION:

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Scarings, Stephen

TITLE REPERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 935948

LENGTH: 19
                                                                                              Sequence 920023, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
FRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-11-14
PRIOR PLILING DATE: 2003-11-14
PRIOR PLILING DATE: 2002-11-14
PRIOR PLILING DATE: 2002-11-14
PRIOR PLILING DATE: 2002-11-14
SPRIOR PLILING DATE: 2002-11-14
SPRIOR PLILING DATE: 2002-11-14
SPRIOR PLILING DATE: 2002-11-14
SEQ ID NO 920023
LEMORTH: 19
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Pred. No. 1.6e+04;
0; Mismatches 2;
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Best Local Similarity 70.6%; Pred. No. 1.6e+04;
Matches 12; Conservative 3; Mismatches 2;
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Best Local Similarity 88.2%;
Matches 15; Conservative
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US-11-083-784-920023
                                                        RESULT 5
US-11-083-784-920023/c
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US-10-914A-163654
US-10-910-914A-163654
Sequence 163654, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: USES TOO SOURCEDSOI
CURRENT PELING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOUTHWARE: PatentIn version 3.3
SEQ ID NO 163654
LENGTH: 20
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Sequence 344929, Application US/10310914A
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Pred. No. 1e+04;
2; Mismatches 3; Indels (
                                                                                                                                                                                                       Score 14.6; DB 11; Length 22; Pred. No. 6.5e+03;
                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                 Query Match 66.4%; Score 14.6; D
Best Local Similarity 61.9%; Pred. No. 6.5e
Matches 13; Conservative 4; Mismatches
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1053240
LENGTH: 22
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Best Local Similarity 73.7
Matches 14; Conservative
                                                                                                ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053240
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Human
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Indels

Length 19;

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Length 19;

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Sequence 353174, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwinton:
ITILE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
ITILE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 353174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-310-914A-805859/c
US-10-310-914A-805859/c
US-10-310-914A-805859/c
US-10-310-914A-805859/c
US-10-310-914A-805859/c
US-10-914A-805859, Application US/10310914A

Sequence 805859, Application No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof
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Sequence 353175, Application US/10310914A

GENERAL INFORMATION:

APPLICANT: Bentwich.

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087,0200,CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A
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88.2%; Pred. No. 1.6e+04;
tive 0; Mismatches 2;
1 | |::||| |:|||||
1 CAAGUUACAUGUAGAAA 17
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Best Local Similarity 88.2
Matches 15; Conservative
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US-10-310-914A-353174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
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                                                                                                                                                                                 Sequence 92023, Application US/11101244

Publication No. US2005046794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Characon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Maraball, William
APPLICANT: Scaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional giRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 920023
LENGTHA: 19
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| Sequence 935948, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Marshall, William
| APPLICANT: Laske, Devin
| APPLICANT: Laske, Devin
| APPLICANT: Marshall, William
| PRICANT: Marshall, William
| FILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: 60/502,050
| PRIOR APPLICATION NUMBER: 60/502,050
| PRIOR PILING DATE: 2003-01-07
| PRIOR PILING DATE: 2003-11-14
| SOFTWARE: Proprietary
| SEQ ID NO 935948
| LENGTH: 19
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88.2%; Pred. No. 1.6e+04;
iive 0; Mismatches 2;
                           1 CAAGUUACAUGUAGAAA 17
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Matches 15; Conservative
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Best Local Similarity 70.6
Matches 12; Conservative
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CORGANISM: Homo sapiens
US-11-101-244-920023
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ORGANISM: Homo sapiens
                                                                                                                                                                    US-11-101-244-920023/c
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US-11-101-244-935948
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US-10-914A-574946/c

US-10-916-914A-574946/c

Sequence 574946, Application US/10310914A

Sequence 574946, Application US/10310914A

Publication NO. US20060003322A1

Sequence 574946, Application US/10310914A

Publicant: INFORMATION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: USES thereof

TITLE OF INVENTION: USES thereof

TITLE REPERRORS: 06087,0200.CPUS01

FILE REPERRORS: 06087,0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: ParentIn version 3.3

SEQ ID NO 574946
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Sequence 361013, Application US/10310914A
Sequence 361013, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 361013
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93.3%; Pred. No. 2.5e+04;
iive 0; Mismatches 1;
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Pred. No. 3.1e+04;
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Job time : 858 secs
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Best Local Similarity 83.3%;
Matches 15; Conservative
                7 ACAGGGAGAAAAGCC 21
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Best Local Similarity 93.3
Matches 14; Conservative
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; ORGANISM: Human
US-10-310-914A-574946
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US-10-310-914A-361013
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Publication No. US20060003322A1
Publication No. US20060003322A1
Publication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT PRILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ TWARET: 19
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| Publication No. US20060003322A1
| GENERAL INRORMATION:
| APPLICANT: Shiler, Kvuzat
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06087.0200.CPUS01
| CURRENT APPLICATION WUMBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 46518
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3 UGUUACAGGAAGAGAAG 19
CURRENT FILING DATE: 2002-12-(
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 353175
LENGTH: 22
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Best Local Similarity 86./-
                                                                                                                                                                                                                    Query Match 62.7
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                         GRGANISM: Human
US-10-310-914A-353175
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US-10-310-914A-117024
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US-10-310-914A-464518
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-310-914A-117024
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                                                                                                                             TYPE: RNA
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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

applications make up the Published Applications Main databases. Mewly publications make up the Published Applications May published Applications make up the Published Applications May published Applications and Applications May published Applications May be a subject of the Published Applications and Applications May provide the Published Applications May provide the Published Applications and Applications May provide the Published Application

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions arm of the control o

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Query Match
Best Local Similarity
Matches 14; Conserv
; ORGANISM: HUMAN
US-11-242-111-36
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APP
APP1
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12, Appl
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Sequence 30, Appl
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Appl
                                                                                                                    June 8, 2006, 22:49:54; Search time 23 Seconds (without alignments) 121.405 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA New:*

1: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US08_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptcdata/2/pubpna/US10_NEW_PUB.seq:*
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               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-293-697-5192
US-11-293-697-527
US-11-293-697-529
US-11-293-697-5086
US-11-255-980-60
US-11-251-465-425
US-11-251-465-425
US-11-251-465-426
US-11-251-465-426
US-11-293-697-5096
US-11-291-697-9983-38
US-11-293-697-5297
US-11-267-9383-38
US-11-293-697-5297
US-11-267-937-1889
US-11-267-937-1889
US-11-264-737-112
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US-10-511-455-77
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 22
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Match
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Perfect score:
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APPLICANT: Lee, Nancy M
TITLE OF INVENTION: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION
TITLE OF INVENTION: OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF
FILE REFERENCE: NLEE-01001US1 MCP/MLB
CURRENT APPLICATION NUMBER: US/11/242,111
CURRENT FILING DATE: 2005-09-29
PRIOR FILING DATE: 2004-09-30
PRIOR FILING DATE: 2004-09-30
PRIOR PILING DATE: 2005-02-08
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1111, App
1143, App
98, App
1122, App
1122, App
1122, App
119, App
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US-10-511-832-90
US-11-511-937-1865
US-11-078-073-406
US-11-078-073-407
US-10-511-937-868
US-10-514-776-62
US-11-158-209-920
US-11-252-276-111
US-11-252-276-111
US-10-559-415-143
US-00-756-0978-98
US-10-659-938A-122
US-10-659-938A-122
US-11-265-052-19
US-11-265-05-19
US-11-265-05-19
US-11-265-05-19
US-11-265-05-19
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US-11-265-05-19
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APPLICANT: MUNICH, Arnold
ITILE ORD INVENTION: Spinal Muscular Atrophy Districts REFERENCE: 2121-0140P
CURRENT APPLICATION NUMBER: US/11/222,810
CURRENT APPLICATION NUMBER: US/011/09,082
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-05
PRIOR FILING DATE: 1995-10-19
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/11242111 Publication No. US20060088862A1 GENERAL INFORMATION:
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SOFWARE: Patentin version 3.3
SEQ ID NO 3.4
LENCTH: 21
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; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized pr
US-11-293-697-5279
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                                                                                                                                                    Length 21;
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                                                                                                                                                                                               Indels
                                                                                                                                                  Score 10.8; DB 6;
Pred. No. 3.9e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/11189279
Publication No. US20060115829A1
GENERAL INFORMATION:
APPLICANT: MAO, LI
APPLICANT: WANG, JIE
APPLICANT: WANG, JIE
APPLICANT: WANG
TITLE OF INVENTION: A METHOD OF TREATING CANCER
FILE REFERENCE: UTXC:875US
CURRENT APPLICATION NUMBER: US/11/189,279
CURRENT PRILING DATE: 2005-07-26
PRIOR PILING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 44
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5279, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR PAPLICATION NUMBER: US/10/108,260
PRIOR PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENT NOS: 5458
SOFTWARE: PATENT NOS: 5458
SOFTWARE: PATENT NOS: 5458
SOFTWARE: PATENT NOS: 5458
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          8 ACAGGTAGAAAGC 21
                                                                                                                                                                                                                                                                                      20 ACAGGTAAGAAGC 7
                                                                                                                                             Query Match
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 76.5'
Matches 13; Conservative
                                                    TYPE: DNA
CRGANISM: Homo sapiens
US-10-511-937-1101
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Best Local Similarity
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           SEQ ID NO 1101
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                                   LENGTH: 21
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Wordward, MacDonald
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: AND WOMBER: US/10/511,937
CURRENT PILING DATE: 2004-10-19
FRIOR APPLICATION NUMBER: US 10/131,831
FRIOR APPLICATION NUMBER: US 10/131,831
FRIOR APPLICATION NUMBER: US 10/325,899
FRIOR SEQ ID NOS: 3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                   Length 22;
                                                                                                                                                                                                             Indels
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                                                                                                                                                              50.0%; Score 11; DB 7; Le
100.0%; Pred. No. 3.2e+03;
tive 0; Mismatches 0;
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Pred. No. 3.8e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5192, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
    APPLICANT: HELLX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; TITLE OF INVENTION: Novel full length cDNA
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; TITLE OF SEQUENCE 2005-12-05
; FININ A.PLICATION NUMBER: US/10/108,260
; PRIOR PILING DATE: 2002-03-28
; NUMBER: OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5192
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1101, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 85.7*
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                  22 CATGITACAGG 12
                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-11-222-810-30
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                     SEQ ID NO 30
LENGTH: 22
                                               LENGTH:
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APPLICANT: HSIANG, York
APPLICANT: HSIANG, Alison
APPLICANT: BUCHAN, Alison
APPLICANT: BUCHAN, Alison
APPLICANT: BUCHAN, Alison
APPLICANT: BUCHAN, Alison
APPLICANT: MARGARON, Philippe Maria Clotaire
TITLE OF INVENTION: SELECTIVE TREATMENT OF ENDOTHELIAL SOMATOSTATIN RECEPTORS
FILE REPERENCE: 246 52001101
CURRENT APPLICATION NUMBER: US 09/797,779
FRIOR APPLICATION NUMBER: US 09/797,779
FRIOR PLING DATE: 2001-03-01
FRIOR PELING DATE: 1999-00-01
FRIOR PELICATION NUMBER: CA 2,246,791
FRIOR FILING DATE: 1998-09-01
FRIOR PELING DATE: 1998-09-01
FRIOR PELING DATE: 1998-09-01
FRIOR PELING DATE: 1998-09-01
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FRIOR FILING DATE: 1998-09-01
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APPLICANT: SWALSKY, PATRICIA
TITLE OF INVENTION: ENHANCED AMPLIFIABILITY OF MINUTE FIXATIVE-TREATED
TITLE OF INVENTION: TISSUE SAMPLES, MINUTE STAINED CYTOLOGY SAMPLES, AND
TITLE OF INVENTION: OTHER MINUTE SOURCES OF DNA
TITLE OF INVENTION: OTHER MINUTE SOURCES OF DNA
TITLE TELE REFERENCE: 47030.0014-01US
CURRENT APPLICATION NUMBER: 0211/255,980
CURRENT PILING DATE: 2005-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 44.5%; Score 9.8; DB 7; Length 20; Best Local Similarity 84.6%; Pred. No. 1.2e+04; Matches 11; Conservative 0; Mismatches 2; Indels
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PRIOR FILING DATE: 2005-05-12
PRIOR FILING DATE: 2005-05-12
PRIOR PLING DATE: 2005-05-12
PRIOR PLING DATE: 2005-01-19
PRIOR APPLICATION NUMBER: 60/644, 568
PRIOR PILING DATE: 2005-01-19
PRIOR PILING DATE: 2004-11-29
PRIOR PLING DATE: 2004-11-29
PRIOR PILING DATE: 2004-11-29
PRIOR PILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN NUMBER: 60/620, 926
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET: 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Human SSTR3 primer US-11-189-597-5
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                                                                                                         Sequence 5, Application US/11189597
Publication No. US20060089299A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
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1; Indels
                                                                                                                                                                                                                             US-11-264-558-29/C

US-11-264-558-29/C

Sequence 29, Application US/11264558

Publication No. US2006008913A1

GENERAL INFORMATION:
APPLICANT: Bionomics Limited
APPLICANT: Mallace, Robyn H
APPLICANT: Mallacy, John C
APPLICANT: Mallacy, John C
APPLICANT: Harkin, Louise A
APPLICANT: Harkin, Louise A
APPLICANT: Berkovic, Samuel F
APPLICANT: Berkovic, Samuel F
APPLICANT: BARKIN, Louise A
APPLICANT: BARKIN, Louise A
APPLICANT: BARKIN: Louise A
APPLICANT: DARKIN MUMER: US/11/264,558
CURRENT FILING DATE: 2005-11-01
RRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 29
LENGTH: 22
LENGTH: 22
LENGTH: 22
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Sequence 5086, Application US/11293697

Sequence 5086, Application US/11293697

GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length CDNA

FILE REPERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT PILING DATE: 2005-12-05

PRIOR PELING DATE: 2005-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PATENTIN VOICE: 21

SOFTWARE: PATENTIN VOICE: 21

SOFTWARE: PATENTIN VOICE: 21

SOFTWARE: PATENTIN VOICE: 21

SERVICE THE STATE OF SEQ ID NOS: 5458

LENGTH: 18
Mismatches
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ORGANISM: Artificial Sequence
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11; Conservative
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; ORGANISM: Homo sapiens
US-11-264-558-29
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Matches
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Sequence 426, Application US/11251465
Sequence 426, Application US/11251465
Sequence 426, Application No. US20060094061A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Tomme, Peter
APPLICANT: Tasassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: 1012-A USA
CURRENT PALLICATION NUMBER: US/11/251,465
CURRENT PAPLICATION NUMBER: 2005-10-14
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SEQ ID NO 426
LENGTH: 21
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Sequence 38, Application US/10148883

Sequence 38, Application US/10148883

Publication No. US20060115811A1

GENERAL INFORMATION:

APPLICANT: Jay White et al.

TITLE OF INVENTION: Cytochrome P450RA1-2 and Related Proteins

FILE REFERENCE: 1812-49

CURRENT APPLICATION NUMBER: US/10/148,883

CURRENT FILING DATE: 2003-02-13

PRIOR APPLICATION NUMBER: US 60/171,110

PRIOR APPLICATION NUMBER: US 60/171,110

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 40

SOSTWARE: Patentin Version 3.3

SEQ ID NO 38

LENGTH: 22
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43.6%; Score 9.6; DB 6; Length 22;
Best Local Similarity 75.0%; Pred. No. 1.6e+04;
Matches 12; Conservative 0; Mismatches 4; Indels
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Publication No. US20060105376A1
GENERAL INFORMATION:
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Best Local Similarity 75.04
Matches 12; Conservative
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US-10-148-883-38
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sequence 425, Application US/11251465
sequence 425, Application No. US20060094061A1
sequence 425, Application No. US20060094061A1
sequence 425, Application No. US20060094061A1
septicant: Brys. Reginald
septicant: Towne, Peter
septicant: Towne, Peter
septicant: Towne, Peter
septicant: Title OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
string OF INVENTION: Inflammatory Diseases
string OF INVENTION: Inflammatory Diseases
string DATE: 2003-10-14
sprior Filing DATE: 2004-10-15
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Query Match

44.5%; Score 9.8; DB 7; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.2e+04;
Matches 11; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.2e+04;
0; Mismatches 2; Indels
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; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-425
                                                                                                                                                                                                                                      RESULT 11
US-10-559-415-155/c

Sequence 155, Application US/10559415
PUDLication No. US20060100132A1
GENERAL INFORMATION:
APPLICANT: ABtraZeneca AB et al
TITLE OF INVENTION: Diagnostic Method
FILE REFERENCE: 101073-1P WO
CURRENT FILING DATE: 2005-12-06
FRIOR APPLICATION NUMBER: US/10/559,415
CURRENT FILING DATE: 2005-12-06
FRIOR APPLICATION NUMBER: 0313081.2
FRIOR FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 191
SEQ ID NO 155
LENGTH: 21
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1 Similarity 84.6%;
11; Conservative (
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ORGANISM: Artificial Sequence
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                                                                                                          1 GCATGTTACAGGT 13
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                                                                                                                                                                  19 GCATATTACTGGT 7
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US-10-559-415-155
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Best Local Similarity
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Best Local Similarity
Matches 11, Conserva
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US-11-251-465-425
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TITLE OF INVENTION: Novel full length cDNA
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCES: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT PELLING DATE: 2005-12-05
FRIOM FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5297
TYPE: DNA
TYPE: DNA
FIRMANISM: Artificial Sequence
FRATUR: FRATURE:
FRATUR:
GRANISM: Artificial Sequence
FRATUR:
GRANISM: OTHER INPORMATION: Description of Artificial Sequence: an artificially synthesized FUS-11-293-697-5297
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42.7%; Score 9.4; DB 7; Length 18;
Best Local Similarity 90.9%; Pred. No. 1.9e+04;
Matches 10; Conservative 0; Mismatches 1; Indels
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Searched:

Database

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AR104505 Sequence
AX972882 Sequence
CS018067 Sequence
CS018067 Sequence
AR0231719 Sequence
AR02390 Sequence
AR05390 Sequence
BD067607 Enzymatic
122067 Sequence
AR327065 Sequence
AR377836 Sequence
AR371836 Sequence
AR371836 Sequence
AR371835 Sequence
AX310829 Sequence
AX310829 Sequence
AX310829 Sequence
CZ7555 Canis famil
CG76685 Sequence
BD176954 Novel pro
BD016954 Novel pro
BD016954 Novel pro
BD016894 Novel pro
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Pred. No. 1.1e+05;
0; Mismatches 0; Indels
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Buell, G.Nutter., Surprenant, A. and Kawashima, B. Purinergic receptor
Patent: US 6133434-A 3 17-OCT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
1 (bases 1 to 20)
Buell,G.N., Surprenant,A. and Kawashima,E.
                                                                                                                                                                                                                                                                     DNA
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                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
/mol_type="unassigned DNA"
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6509163.
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BD067607
AR327036
AR402107
AX217836
AR160744
AR110829
BD138283
BD138283
BD178555
AX804694
CQ786688
BD0176594
BD0176594
BD0176594
BD015694
BD015694
AX690585
AR070817
AR104505
AX962823
AX737882
CS018067
CS018067
CS037179
AR328335
AR007304
AR007309
                                                                                                                                                                                                                                                                                                                                                                                                        61.9%; Score
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR275648
Sequence 3 from patent US
AR275648
AR275648.1 GI:29709099
                                                                                                                                                                                                                                                                                           AR116690.1 GI:14097012
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGTATCTGAAG 13
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AR116690
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AR275648
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AR275648 Sequence
BD0675608 Enzymatic
AR402108 Sequence
A17234 Oligonucleo
AR027617 Sequence
DD266720 RNA Inter
DD266722 RNA Inter
DD26732 RNA Inter
DD26732 RNA Inter
DD266736 RNA Inter
DD267467 RNA Inter
DD20747 RNA Inter
DD207477 RNA Inter
BD67609 Enzymatic
AR402109 Sequence
                                                            (without alignments)
671.112 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                  8, 2006, 23:04:25; Search time 2001 Seconds
      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                        1150878
                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                        6366136 segs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                           AR275648
BD067608
AR02108
A17234
AR027617
AR027617
DD206728
DD206732
DD206732
DD206732
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DD206744
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gb_p1: *
gb_pr: *
gb_r: *
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Maximum DB seq length: 21
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PAT 29-SEP-1999
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                                                                                      1 (bases 1 to 17)
McMathar, S., Fell, P. and McSwiggen, J.A.
Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors
Patent: US 6623962-A 448 23-SER-2003,
Sirna Therapeutics, Inc. and Aston University; Boulder, CO
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
Unclassified.
1 (bases 1 to 20)
Craig,S., Hunter,M.George., Edwards,R.Mark., Czaplewski,L.George. and Gilbert,R.James.
Stem cell inhibiting proteins
Stem cell inhibiting proteins
Patent: US 5856301-A 134 05-JAN-1999;
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A17234 20 bp DNA linear Oligonucleotide 20-mer BB9513 (SEQ ID NO: 134).
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20)
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Patent: WO 9313206-A 134 08-JUL-1993;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 bp DN Sequence 134 from patent US 5856301. AR027617.
                                                                                                                                                                                                                                 /organism="unknown"
/mol_type="genomic DNA"
   AR402108.1 GI:40149558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGGCGTATCTGAAGA 16
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                                                                       Unclassified.
                                    Unknown,
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AR027617/c
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A17234/c
LOCUS
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unclassified sequences.

I (bases 1 to 17)

S Akhtar, S., Pell, P. and Mcswiggen, J.A.

Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors

Lo levels of epidermal growth factor receptors

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
OS Unidentified
PP 14-1AN-1999 BP 1998532913
PP 14-1AN-1999 BP 1998532913
PR 31-JAN-1997 US 60/036476, 04-DEC-1997 US SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC C12N99/00. COTMAIA/71

CC Strandedhess: Single;
CC TOPOLOGY: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
                                                                                                                                                                                                                                                                                                                                                              Encyporal Description of England Books or Conditions related to levels of epidermal growth factor receptors.

BD067608.1 G1:22613211
UP 200151103-A/448.
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Enzymatic nucleic acid treatment of diseases or conditions related to
levels of epidermal growth factor receptors
Key
Location/Qualifiers
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Methods of screening modulators of mammalian P2X7 purinergic
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                                                                                                                                                                                          Query Match 61.9%; Score 13; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 13; Conservative 0; Mismatches 0; Indels
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Sequence 448 from patent US 6623962.
AR402108
              receptors
Patent: US 6509163-A 3 21-JAN-2003;
Glaxo Group Limited; Middlesex;

    .17
    /organism="unidentified"
    /mol_type="genomic RNA"
    /db_xref="taxon:32644"

    .20
    /organism="unknown"
    /mol_type="genomic DNA"

                                                                                      Location/Qualifiers
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REFERENCE AUTHORS TITLE

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SM synthetic construct
other sequences; artificial sequences.

1 (Dases 1 to 21)

8.8 Beigelman, L. and Mcswiggen, J.

RNA Interferrence Mediated Inhibition of BCL2 Gene Expression Using
Short Interferring Nucleic Acid (siNA)
Patent: JP 2005517452-A 841 16-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
PN JP 2005517452-A/841
PD 16-JUN-2005
PR 18-JUN-2005
PR 18-JUN-2005
PR 15-JAN-2003 US 60/440129, 09-SEP-2002 US 60/409293, PR 15-JAN-2003 US 60/440878, PR 16-JUN-2002 US 60/365184, PR 18-JUL-2002 US 60/363124, 20-FEB-2002 US 60/363800 PI leonid beigelman, james mcswiggen

CC Description of Artificial Sequence: siNA sense region FH Key
                                                                                              Sirna Therapoutics Inc.

S Artificial Sequence

PN JP 2005517452-A/837

PD 16-JUN-2005

PP 18-FEB-2003 JP 2003569860

PR 15-JAN-2003 US 60/409293, PR 15-JAN-2003 US 60/409293, PR 18-JUL-2002 US 60/409293, PR 18-JUL-2002 US 60/386784, PR 11-JUL-2002 US 60/386782, PR 11-JUL-2002
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21 bp RNA linear PAT 19-JAN-2000 RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA).
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/note='3'-3 attached terminal deoxyabasic
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/note='5'-3 attached terminal deoxyabasic
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hote=2'. deoxy-2'-fluoro'

(20). (21)

hote='n stands for thymidine' FT
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/note='n stands for thymidine'
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'
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              Short Interfering Nucleic Acid (siNA)
Patent: JP 2005517452-A 837 16-JUN-2005;

    .21
    ^organism="synthetic construct"
|mol_type="unassigned RNA"
|db_xref="taxon:32630"

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other sequences, artificial sequences.

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RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interference Mediated Inhibition of Sina Interference Mediated Inhibition Of Sina Interference Interference Mediated Inhibition Of Sina Interference Inte
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1 (bases 1 to 21)
Beigelman, L. and Mcswiggen, J.
RNA Interference Mediated Inhibition of BCL2 Gene Expression Using
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61.0%; Score 12.8; DB 2;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2;
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    /organism="synthetic construct"
|mol_type="unassigned RNA"
|db_xref="taxon:32630"

/organism="unknown"
/mol_type="unassigned DNA"
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cheses artificial sequences.

It bases 1 to 21)

Beigelman, L. and Mcswiggen, J.

RNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA)

La Patent: JP 2005517452-A 849 16-JUN-2005;

Sina Therapeutics Inc
OA Artificial Sequence
NO Artificial Sequence (0/400293, PR 15-JAN-2003 US 60/400129, 09-SEP-2002 US 60/400293, PR 15-JAN-2003 US 60/400378, 29-AUG-2002 US 60/36095, 06-JUN-2002 US 60/36095, 06-JUN-2002 US 60/36095, 06-JUN-2002 US 60/36095, 06-JUN-2002 US 60/360905, 06
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21 bp RNA linear PAT 19-JAN-2006 KNA Interference Mediated Inhibition of BCL2 Gene Expression Using Short Interfering Nucleic Acid (siNA).
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/note='n stands for thymidine'
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/note='2'-deoxy'
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy'
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro
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llarity 87.5%; Pred. No. 1.40+05;
Conservative 0; Mismatches 2;
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/note='2'-deoxy'
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S Beigelman, L. and Mcswiggen, J.
S Beigelman, L. and Mcswiggen, J.
S Beigelman, L. and Mcswiggen, J.
C Britarier construction of BCL2 Gene Expression Using
Short Interfering Nucleic Acid (siNA)
L Patent: JP 2005517452-A 845 16-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
NN JP 2005517452-A/845
PD 16-JUN-2005
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Key
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61.0%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels
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PR 15-JAN-2003 US 60/440129, 09-SEP-2002 US

05-SEP-2002 US 60/408378, 29-AUG-2002 US 60

18-UUL-2002 US 60/396905, 06-UUN-2002 US 60

11-MAR-2002 US 60/363124, 20-FEB-2002 US 60
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'
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                                       1.21
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_kref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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other sequences; artificial sequences.

1 (bases 1 to 21)
Jumison, S., Posunafu, C., Beigelman, L., Chourira, B., Thompson, J.,
Asuman, N., Pavco, P. and Mcswiggen, J.
RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA)
Patent: JP 2005518803-A 259 30-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
RN JP 2005518803-A/259
PD 30-JUN-2005
PP 20-FEB-2003 JP 2003573107
PR 15-JAN-2003 US 60/440129, 09-SEP-2002 US 60/409293, PR
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60/406784, PR
60/363124, PR
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/note='5'-3 attached terminal deoxyabasic
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/note='3'-3 attached terminal deoxyabasic
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60/363124, PR
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//note='2'-deoxy-2'-fluoro'

/20). (21)

/note='n stands for thymidine' FT
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/note='2'-deoxy-2'-fluoro'
(5). (9)
/note='2'-deoxy-2'-fluoro'
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60/386782,11-MAR-2002 US
60/358580
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          Patent: JP 2005518803-A 256 30-JUN-2005;

    .21
    forganism="synthetic construct"
mol type="unassigned RNA"
|db_xref="taxon:32630"

                      Sirna Therapeutics Inc.
OS Artificial Sequence
PN JP 2005518803-A/256
PD 30-JUM-2005
PP 20-FEB-2003 JP 2003573107
PR 15-JAM-2003 US 60/40129
OS-SEP-2002 US 60/386782,11-M
20-FEB-2002 US 60/38580
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06-JUN-2002 US
20-FEB-2002 US
PI sharon jami
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chourira,
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synthetic construct
other sequences; artificial sequences.
Jakasea I to 21)
Jamison, S., Fosunafu, C., Beigelman, L., Chourira, B., Thompson, J.,
Asuman, N., Pavco, P. and Mcswiggen, J.
RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA)
                                 synthetic construct
synthetic construct
synthetic construct
1 (bases 1 to 21)
Beigelman, L. and Mcswiggen, J.
RNA Interference Mediated Inhibition of BCL2 Gene Expression Using
Short Interfering Nucleic Acid (siNa)
Patent: JP 2005517452-A 853 16-JUN-2005;
Sirna Therapoutics Inc
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RNA linear PAT 19-JAN-2006

RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA).
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60/386782, PR
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60/358580 PI
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/note='n stands for thymidine' FT
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/note='2'-deoxy-2'-fluoro'
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/note='2'-deoxy-2'-fluoro'
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60/396905, 06-JUN-2002 US
60/363124, 20-FEB-2002 US
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/organism="synthetic construct"
/mol_typo="unassigned RNA"
/db_xref="taxon:32630"
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/note='2'-deoxy'
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/note='2'-de

(16) . . (16)

/note='2'-de

(17) . . (18)

/note='2'-de
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PN JP 2005517452-A/853
PP 16-JUN-2005 JP 2003569860
PR 15-JAN-2003 US 60/440129,
OS-SEP-2002 US 60/396905, 06-JI
11-MAR-2002 US 60/36318, 29-AI
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/note='2'-de
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CC Description of Artifi
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JP 2005518803-A/256.
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other sequences; artificial sequences.

1 (bases 1 to 21)
Samison,S., Fosunafu,C., Beigelman,L., Chourira,B., Thompson,J.,
Asuman,N., Pavco,P. and Mcswiggen,J.
RNA Interference Mediated Inhibition of Gene Expression Using Short
Interfering Nucleic Acid (siNA)
L Patent: JP 2005518803-A 262 30-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
PN JP 2005518803-A/262
PD 30-JUN-2005
PF 20-FEBB-2003 JP 2003573107
PR 15-JAN-2003 US 60/440129,09-SEP-2002 US 60/409293, PR
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RNA Interference Mediated Inhibition of Gene Expression Using Short Interfering Nucleic Acid (siNA).
PI james thompson, nashimu asuman, pamela pavco, james mcswiggen CC Description of Artificial Sequence: siNA antisense region FH Key
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60/406784, PR
60/363124, PR
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'note='Phosphorothioate 3'-Internucleotide
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/note='n stands for thymidine' FT
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/note='n stands for thymidine'
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/note='2' deoxy-2'-fluoro'

(16) . .(16)

/note='2' deoxy-2'-fluoro'

(19) . .(19)

/note='2' deoxy-2'-fluoro'
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                                                            (1) . .(1)
/note='2'-deoxy-2'-fluoro'

    .21
    forganism="synthetic construct"
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|db_xref="taxon:32630"

    .21
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|db_xref="taxon:32630"

                                                                                                                                                                                                                                                                                          Location/Qualifiers
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JP 2005518803-A/262.
synthetic construct
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                                    Key misc_feat
FT misc_feat
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DD207473
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Gaps
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Best Local Similarity 87.5%; Pred. No. 1.4e+05; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                        Search completed: June 8, 2006, 23:38:04
Job time : 2003 secs
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                                                                       4 GTCTCTGAAGACTCTG 19
                                                   6 GTATCTGAAGAGTCTG
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C00979 HUMGS000336

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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CF325351 JWT1--03-
CM97681 CO7 02547
D20709 HUMGS01665
AJ671616 AJ671616
CO778852 BL004D H0
AZ480596 BM0302D18
AZ658035 IM0534P03
AG194535 Pan trogl
CW986631 KBZH013B0
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AG203835 Pan trogl
AG203835 Pan trogl
AZ787920 ZM0034M09
DW831454 KBFS00810
DX068324 KBFS00810
DX068324 KBFS0077A0
CL694050 PRI0163a
AM075273 AM075273
CL423467 01805577
                                                                                                                                                                                                                                                                                                                                                      AZ784664 16-FEB-200 DNA linear GSS 16-FEB-200 2M0027I10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0027I10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. Slomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Blam, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Bislam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0027 row: I column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
         CF325351

CM497681

D20708

AJ671616

CO778852

AZ480596

AZ68035

AC194535

AC194535

AC194535

AC194535

AC1931835

AC1931834

AC1931835

AC194050

AC1694050

AM075234

ALC623463
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/clone="UUGC2M0027110"
/sex="Male"
                                                                                                                                                                                                                                 AJ588865
AZ358656
BQ595520
                                                                                                                                                                                                                                                                   AZ320114
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                AZ784664.1 GI:12920631 GSS.
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Fax: 801 585 7177
 AZ784664
VERSION
KEYWORDS
SOURCE
ORGANISM
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AZ784664
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CAB51013 D09B11 C1
AZ495849 1M0131N12
AZ457649 2M0130A02
CZ282704 Cp25h01.r
DUB31624 KBES008M0
AZ489135 1M0139H15
CL681189 PR10130b
AZ58384 1M001K17
AZ36384 1M001K17
AZ368747 Azabidops
AJ684587 Azabidops
AJ684587 Azabidops
AJ685776 1M0465C08
BG924548 HNC27-1-G
AJ525876 Azabidops
AJ525876 Azabidops
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                                                                  June 8, 2006, 23:04:50 ; Search time 2506 Seconds (without alignments) 468.598 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                       48236798 seqs, 27959665780 residues
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AA592729
CA851013
AZ495849
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CZ282704
DU831624
AZ489135
CL681189
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AZ308384
AZ308387
AZ48587
AZ684587
AZ685786
BG924548
AZF52576
                                                - nucleic search, using sw model
                                                                                                                                   1 ctggcgtatctgaagagtctg 21
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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9b_est3:.*
9b_est5:.*
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Result

AJ588865 Arabidops AZ358656 IM0101K12 BQ595520 B012693-0 AZ320114 IM0040D05

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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by respected bases and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb) AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent B. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Exty cedex, RRANGE
Gaston Cremieux, 91057 Exty cedex, RRANGE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.info.gen.fr).
Location/Qualifiers
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Arabidopsis thaliana T-DNA flanking sequence, right border, clone 631B09, genomic survey sequence.
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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="genomic DNA"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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Matches 11; Conserval
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AJS92729/c
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D09B11 C11_04.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D09B11 5', mRNA sequence.
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Alkharouf, M., Khan, R. and Matthews, B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Roots"
/dev stage="Seedlings"
/dev stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ495849 19 bp DNA linear GSS 05-OCT-200
1M0331N22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
/db_xref="taxon:3702"
/clone="631B09"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                              Gaps
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    .15
/note="T-DNA flanking sequence
right border"

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                                                                /ecotype="Wassilewskija"
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D09B11"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil#732114|gplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Damid inserts
C Dupublished (2000)
C Ontact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
           2M0190A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0190A02 R, genomic survey sequence.
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84.6%; Pred. No. 5.4e+06;
tive 0; Mismatches 2; Indels
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Rax: 801 585 7177

Bax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Brror: 0.00

Plate: 0190 row: A column: 02

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.
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organism="Mus musculus"
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/strain="C57BL/6J"
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1 (Dases 1 to 19)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R.; Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.; Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.; Ungublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah

University of Utah
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one UUGC1M0331N22 R, genomic survey sequence.
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/strain="C57BL/6J"
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/clone="UUGC1M0331N22"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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AZ489135 20 bp DNA linear GSS 05-0CT-2000 1M0319H15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0319H15 R, genomic survey sequence.
                                                                                                                                                       /sub species="pakinensis"
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/note="vector: pCUGIBACI; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/note="Tweator: PWD42nv; Purified genomic DNA from M.musculus C57BL/60 (male) was obtained from the Jackson
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Dunn,D., Acyagi,A., Barber,M., Beaccrn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus

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        /organism="Brassica rapa subsp. pekinensis"
        /mol type="genomic DNA"
        /cultivar="Chiffu"

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Pred. No. 5.4e+06;
0; Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0319 row: H column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0319H15"
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ilarity 84.6%;
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      Seq primer: T7
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                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.

1 (bases 1 to 20)

Logue, M.E., Wong, S., Wolfe, K.H. and Butler, G.
A genome sequence survey shows that the pathogenic yeast Candida parapsilosis has a decerve WILal allele at its mating type locus Eukaryot. Cell 4 (6), 1009-1017 (2005)
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Bmall: pbeom@rda.go.kr
BMC end sequence of Brassica rapa 88p. pekinensis Sau3AI BAC clone
KBrS008M03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5480"
/clone="cp25h01"
/clone_lib="Candida parapsilosis Random Genomic Library"
                                                                                                                                                                                                                                                                                                                                                        Contact: Logue M
Department of Biochemistry, Conway Institute of Biomolecular and
Biomodical Research
University College Dublin
Dublin 4, Ireland
Tel: +353 1 7166885
Fax: +353 1 2837211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.
                    cp25h01.r Candida parapsilosis Random Genomic Library Candida
parapsilosis genomic clone cp25h01, genomic survey sequence.
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  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Candida parapsilosis"
/mol_type="genomic DNA"
/strain="CLIB214"
    DNA
20 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mary.e.logue@ucd.ie
Class: plasmid ends.
                                                                                        CZ282704.1 GI:68453906
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                                                                                                                             Candida parapsilosis
Candida parapsilosis
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 47121141gb]AP129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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PRIO130b G06 2 - PRIO130b.BR (17) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic CL681189
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Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (bases 1 to 17)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nuclei Acids Res. 32 (1), D421-D422 (2004)
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
45.7%; Score 9.6; DB 11; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.8e+06;
Matches 12; Conservative 0; Mismatches 4; Indels
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Max-Planck-Institute for Developmental Biology
Spemannatr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db xref="taxon:54126"
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Seq primer: T7
Class: fosmid ends.
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Location/Qualifiers
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Best Local Similarity 90.9°
Matches 10, Conservative
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated epassage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gf of a 9.5 to
10.5 kb range using preparative agarose gf rom a derivative
of pWD42 (gi | 4732114| gb| AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coll XIL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
AZ308384 29-SEP-2000 1M0011K17P Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0011K17 F, genomic survey sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bumanlai; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

(bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Reilly, M., Rose, R., Stokes, R., Stokes, R.,

Reilly, M., Rose, R., Stokes, R.,

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Fail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0011 row: K column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0011K17"
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Location/Qualifiers
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GSS.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Hen. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA
                                                                                                                                                                                                     GSS 29-SEP-2000
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                                                                                                                                                                                                  AZ316351 20 bp DNA linear GSS 29-SEP-200 1M0034A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0034A11 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G79L/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: A column: 11
Seq primer: CGTYCTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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/strain="C57BL/60"
/db_xref="taxon:10090"
/clone="UUGC1M0034A11"
                                                                                                                                                                                                                                                                                                                                                                         musculus (house mouse)
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                                   4 ATCTGAAGTGACCG 17
ATCTGAAGAGTCTG 21
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Gaps

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43.0%; Score 9.2; DB 11; Length 20; 78.6%; Pred. No. 1.1e+07; ive 0; Mismatches 3; Indels

11; Conservative

Best Local Similarity Matches 11; Conserv

Query Match

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Laboratory Mouse DNR Resource
Laboratory Mouse DNR Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor or oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                               AZ328275 29-SEP-2000 1M0052A01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0052A01 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           É
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-" /clone llb="Mouse 10kb plasmid UGGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, D., Adgara, L. C., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Moule whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.8%; Score 9.2; DB 11; Length 20; 78.6%; Pred. No. 1.1e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Pax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: A column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .20
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0052A01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                             AZ328275.1 GI:10387840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
20 ATCTCAAGATACTG 7
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Matches

ò 셤 SOURCE

REFERENCE AUTHORS REFERENCE AUTHORS

PUBMED JOURNAL

TITLE

TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

ò 셤 RESULT 14 AJ684587 LOCUS DEFINITION ACCESSION VERSION

ACCESSION VERSION KEYWORDS

AJ587417/c DEFINITION

RESULT 13

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Anderson, S. I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
(bnpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                         Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transforments of Arabidopsis thalians
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATH524367 18 bp DNA linear GSS 08-FEB-2006
                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone Ilb="CSEGRANO4"
hote="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ524367

AJ524367

AJ524367.1 GI:26792603

Arabidopsis thaliana (thale cress)

Fararyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F., Chavvin, S., Bechlold, N., Craud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T_DNA integration into the Arabidopais genome depends on sequences
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100.0%; Pred. No. 1.3e+07;
ative 0; Mismatches 0;
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EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="uterus"
/clone_Tib="CSEQRAN04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001805 G15"
                                                                                                                                                                          (bases 1 to 16)
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Balzergue, S.
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                                Sus scrofa (pig)
Sus scrofa
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AUTHORS
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Submitted (13-0CT-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue Direct Submission

Submitted (13-0CT-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                    AJS87417 10 bp DNA linear GSS 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO 25 pre-insertion sites
EMBO 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                             AJSB/417.1 GI:37937041
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="275G07"
/clone_lib="Arabidopsis_thaliana T-DNA insertion lines"
        Gaps
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  Indels
  3,
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/mol_type="genomic DNA"
/db_xref="taxon:3702"

    10
    note="T-DNA flanking sequence"

  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ecotype="Wassilewskija"
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AJ684587
AJ684587.1 GI:49417177
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                                                    4 GCGTATCTGAAGAG 17
                                                                                                            19 GCGTACCTGTAAAG 6
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Matches 9; Conservative
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to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dosgap.versailles.lina.fr/publiclines. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).

1. 18

| Program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
| Organism="Ambidopsis thaliana" | Anologen.fr | Anologen.fr
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GenCore version 5.1.9

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2006, 23:38:20 ; Search time 100 Seconds

(without alignments)

392.933 Million cell updates/sec
```

(without alignments)

Title:
US-09-743-825-8

Sequence:
1 ctggggtatctgaagagtctg 21

Scoring table: IDENTITY\_NUC
Gapox 10.0 , Gapext 1.0

Searched: 140366 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 21

538872

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Issued Patents\_NA:\*

1: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/1\_COMB.seq:\*
2: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/5\_COMB.seq:\*
3: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/6\_COMB.seq:\*
4: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/6B\_COMB.seq:\*
5: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/TCOMB.seq:\*
6: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/PCOMB.seq:\*
7: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/PCTUS\_COMB.seq:\*
8: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/PCTUS\_COMB.seq:\*
9: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/PCTUS\_COMB.seq:\*
10: /EMC\_Celerra\_SIDS3/ptcdata/2/ina/pcCMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3, Application US/09638857;
Sequence 3, Application US/09638857;
Satent No. 6509163;
GENERAL INFORMATION;
APPLICANT: BUELL, GARY N.
APPLICANT: SURRENANT, ANNMARIE
APPLICANT: KARASHIMA, ERLC
TITLE OF INVENTION: A PURINERGIC RECEPTOR;
FILE REFERENCE: 1430-160;
CURRENT APPLICATION NUMBER: US/09/638,857;
CURRENT FILING DATE: 2000-08-15;
PRIOR APPLICATION NUMBER: 08/42,079
PRIOR PILING DATE: 1997-04-28;
NUMBER OF SEQ ID NOS: 20

ö

Gaps

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; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-08-842-079-3

Query Match 61.9%; Score 13; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 3.6e+03; Matches 13; Conservative 0; Mismatches 0; Indels

8 8

US-09-638-857-3

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		26	-	٠	ď		10	۳ (	TIS-09-280-805-129	100	
		27		ی د	7		200	۳ د	TIS-09-517-4678-30		
·		28			, L	۱ ۵	20	۳ (	TIS-09-198-4528-2767		
		. 0		9	55	ı (N	000	. ~	US-09-657-289A-12		
			11.6	9	55	. ~	20	· ~	US-10-130-158A-12	Segmence 12, Appl	
			1	9	55.2	~	21	· c	US-09-657-472-1916		
	b		H	4	4	. ~	19	m	US-09-422-978-6486	6486	
Ŭ		33	1.	4	54.3	m	20	~	US-08-602-093-12		
	(*)		11.	4.	54.3	9	20	ო	US-09-906-158-68	68,	
Ü			٠	4.	54.3	6	20	m	US-10-002-623-930	930,	
J	ص د	9	٠	~	53.3	<u>س</u>	11	m	US-08-985-162-450	450,	
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	171	80	::	~	53.	~	11	ß	US-10-156-306B-4879	4879.	
	(۳)	39	11	~	53.3	~	18	m	US-09-422-978-5682	5682	
	4,	40	=======================================	7	53.	<u>«</u>	13	N	US-08-555-678-57		
Ū	Ω.	41	11.	7	53.3		13	m	US-09-422-978-4659	465	
Ü		2	11.	N	53.3		19	<b>~</b>	US-09-696-791-466	466	
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									ALIGNMENTS		
R	RESULT	F.									
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5	9-06	US-08-842-079-3	079	ا ب	-	1					
•-	0 0	sequence	ñ,	App	ŭ;	Application US/U8842079	/so	989	57.07		
••	מול ל	Fatent No. 6133434	ì	6133434 00043810	4 6						
•	5	2	Į.	5	7						
•-	A	APPLICANT:	Ë	BOK	BUELL,	GARY					
••	Ą	APPLICANT:	Ë	SUR	PRE	SURPRENANT,	Z	ANNMARIE	<b>29</b>		
•-	A	APPLICANT:	Ë		ASH.	KAWASHIMA, 1	ERIC				
•	H	TITLE OF INVENTION: A	H	NVEN	TIO	- A	PURI	MERC	PURINERGIC RECEPTOR		
	FI	FILE REFERENCE: 1430-160	FERI	ENCE	ř	130-10	9				
	8	RRENT	API	PLIC	AII	DN NC	MBER	SU.	CURRENT APPLICATION NUMBER: US/08/842.079		
· ••	8	CURRENT FILING DATE: 1997-0	F	LING	PA.	CB: 1	-166	04-28			
. ••	₹	NUMBER OF SEC ID NOS: 20	AC.	SEO	21	SON	20	•			
	S	SOPTWARE: PatentIn Ver		Pate	nt Tr	Ver	2.0	_			
•	SEO	SEC ID NO	6			;		,			
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                                                                                                                                                                     FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-638-857-3
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 448, Application US/08985162
Fatent No. 6057156
FAPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: TO LEVELS OF EDIDERAL GROWTH
TITLE OF INVENTION: A.A.
STREET: 631 West Fifth Street
STREET: 601016 STREET
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                                                                                                                                                                                                                                                                                                                Query Match 61.9%; Score 13; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 3.6e+03; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 448:
SEQUENCE CHARACTERISTICS:
                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.55
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GGCGTATCTGAAG 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCGTATCTGAAG 13
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                      SEQ ID NO 3
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6 GTATCTGAAGAGTCTG 21

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Gaps
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                                                                                                             Sequence 448, Application US/09401063

Fatent No. 6623962

GENERAL INFORMATION:
APPLICANT: Pall, Particia
TITLE OF INVENTION: BIZEMARIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEMASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FATTOR RECEPTORS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stem Cell Inhibiting Proteins 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-450-905B-134/C
Sequence 134, Application US/08450905B
Patent No. 5856301
GENERAL INFORMATION:
PAPLICANT:
TITLE OF INVENTION: Stem Cell Inhibit
NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FSELSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: WATADALOR; RICHARIGA J.
REFERENCE/DOCKET NUMBER: 33,327
REFERENCE/DOCKET NUMBER: 33,327
REFERENCE/DOCKET NUMBER: 33,327
REFERENCE/DOCKET NUMBER: 330/107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GTATCTGAAGAGTCTG 21
16 GTATCGAAAGAGTCTG 1
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
                                                                                                 US-09-401-063-448/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-401-063-448
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Length 20;
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Patent No. 6057156

GENERAL INFORMATION:

APPLICANT: Achtar, Saghir

APPLICANT: Rell, Patricia

APPLICANT: Rell, Patricia

TITLE OF INVENTION: ENZYMEATIC NUCLEIC ACID TREATMENT

TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH

TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH

TITLE OF INVENTION: PACTOR RECEPTORS

NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS: 1877

ADDRESSER: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,759F
FILING DATE: 08-MAR-1993
FILING DATE: 08-MAR-1993
FILING DATE: 08-MAR-1993
FILING DATE: 08-MAR-1991
FILING DATE: 23-DEC-1991
FILING DATE: 13-DEC-1991
FILING DATE: 14-DEC-1991
FILING DATE: 14-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102378.120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 1..20
; OTHER INFORMATION: /product= "BB9513 oligomer"
US-07-982-759F-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.0%; Score 12.8; DB 3;
87.5%; Pred. No. 4.5e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
FILING TARESFITCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-226-5000
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGGCGTATCTGAAGA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 CTGACGCATCTGAAGA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.0
Best Local Similarity 97.5
Matches 14, Conservative
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                                                                                                                                                                                                       CUMPRATING SYSTEM; PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,905B
FILING DATE: 26-MAR-1995
RIOR APPLICATION NUMBER: 07/982,759
FILING DATE: 08-MAR-1993
PRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FILING DATE: 108-MAR-1991
PRICH APPLICATION DATA:
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-OCT-1992
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102.378.120DV-2
TELEPHONE: 617-526-6110
TELECOMMUNICATION INPORMATION:
TELEPHONE: 617-526-500
INPORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CRAIG, Stewart
APPLICANT: CRAIG, Michael
APPLICANT: GEORGE, Michael
APPLICANT: GEORGE, Michael
APPLICANT: CZAPLEWSKI, Lloyd George
APPLICANT: CZAPLEWSKI, Lloyd George
APPLICANT: GILBERT, Richard
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: 1..20
CHER INFORMATION: /product= "BB9513 oligomer"
VS-08-450-95B-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-982-759F-134/c
; Sequence 134, Application US/07982759F
; Patent No. 6057123
; GENERAL INFORMATION:
                                                                                             STATE: MA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGGCGTATCTGAAGA 16
CORRESPONDENCE ADDRESS:
ADDRESSER: HALE and DORR
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 creacecarcreaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                    4 GCGTATCTGAAGAGTCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CGTATCTGAAGAGTCTG 21
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
            TYPE: nucleic acid
                              STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 14603
                                                          ; TOPOLOGY:
US-09-401-063-449
                                                                                                                                                                                                                                                                                                                                                                                 US-08-717-291-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-717-291-8
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SETTLE OF INVENTION OF DISEASES OR CONDITIONS RELATED TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED TITLE OF INVENTION: PACTOR RECEPTORS NUMBER OF SEQUENCES: 1877

SCREEPONDENCE ADDRESS: ADDRESS: ADDRESSE: Lyon & Lyon STREET: Saife 4700

STREET: Suite 4700

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORDED
COMPUTER: ELORAGE
COMPUTER: ELORAGE
COMPUTER: ELORAGE
COMPUTER: EASTERN: IBM P.C. DOS 5.0
SOFTWARE: FASTERN: IBM P.C. DOS 5.0
SOFTWARE: PASTERN: DATA:
CLASSIFICATION NUMBER: US/09/401,063
FILING DATE: Q1 December 1997
APPLICATION NUMBER: 08/985,162
RILING DATE: Q4 December 1997
APPLICATION NUMBER: G6/036,476
FILING DATE: 31 January 1997
ATTORNEY AGENT INFORMATION:
                                           REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,0107
TELECOMMUNICATION INFORMATION:
TELEFORM (213) 955-0440
TELEFAK: (213) 955-0440
TELEFAK: (213) 955-0440
TELEFAK: (213) 955-0440
TELEFAK: (213) 955-046
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TYPE: TOPOLOGY: linear
US-08-985-162-449
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REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 230/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 449: SEQUENCE CHARACTERISTICS: LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GCGTATCTGAAGAGTCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GGGTATCGAAAGAGTCT 1
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Best Local Similarity 82.4°
Matches 14; Conservative
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Query Match 58.1%; Score 12.2; DB 3; Length 17; Best Local Similarity 82.4%; Pred. No. 8.9e+03; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.1%; Score 12.2; DB 2; Length 20; Best Local Similarity 82.4%; Pred. No. 9.1e+03; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cesaman, Ethel
APPLICANT: Arvanitakis, Leandros
APPLICANT: Arvanitakis, Leandros
APPLICANT: Arvanitakis, Leandros
APPLICANT: Mossi, Ennouse,
APPLICANT: Mesri, Enrique
TITLE OF INVENTION: KSHV POSITIVE CELL LINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
ATTONREY, AGENT INFORMATION:
NAME: BRAWAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08728603; Patent No. 6093806; GENERAL INFORMATION: APPLICANT: Cesarman, Ethel
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; Sequence 73, Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
; TITLE PREFERENCE: RTS-0109
; CURRENT APPLICATION NUMBER: US/09/433,699B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 73
; LENGTH: 20
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PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED HERPESVIRUS
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Pred. No. 1.1e+04;
0; Mismatches 5; Indels
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                         TITLE OF INVENTION: HEREBOALLO.

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STRET: Clinton Square, P.O. Box 1051
CITY: ROCCHETET
CITY: New York
CONFUTR: USA
ZIP: 14603
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYRE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
SOCTHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PFLICATION NUMBER: US/08/728,603
FILING DATE: 10-OCT-1996
CLASSIFICATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REFERENCE COMMUNICATION INFORMATION:
NAME: BRAMAN, SUSAN J.
REJECTHATION NUMBER: 34,103
REPERENCE CARACTERISTICS:
TELEFOMNINICATION NUMBER: 34,103
REPERENCE TIC-263-1636
TELEFAM: 716-263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENT: NUMBER: 20 base pairs
WUDE: NUMBER: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.1%; Score 12.2; DB 3; Best Local Similarity 82.4%; Pred. No. 9.1e+03; Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Antisense Oligonucleotide US-09-433-699-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.1%; Score 12; DB Best Local Similarity 75.0%; Pred. No. 1.1e Matches 15; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-728-603-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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APPLICANT: McGwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Bacobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions RC
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPRENCE: MBHBOO, 876-J (237/198)
CURRENT FILING DATE: 1999-08-10
PRIOR PLING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
LENGTH: 16
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Sequence 5737, Application US/10138674B

Patent No. 7034009

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Bavco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, James

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Uswells of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Uswells of Vascular Signature of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT APPLICATION UNDMER: US/10/138,674B

CURRENT PILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20829

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5737

LENGTH: 16

TITLE OF INVENTION: DEVELOR OF THE TREATMENT OF THE TREATMENT
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Pred. No. 1.4e+04;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%; Score 11.8; DB 5; Length 16; 73.3%; Pred. No. 1.46+04; ive 2; Mismatches 2; Indels
US-09-371-772B-5737
Sequence 5737, Application US/09371772B
PRETAIN NO. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.;
APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/07852260; Patent No. 5525715
GENERAL INFORMATION:
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Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73.3'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-138-674B-5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-371-772B-5737
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APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Tatem, Joanne M.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/852,260

FILING DATE: 19920619

CLASSIFICATION: 435

ATTORNEY/AGENT INPORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 36607-B-PCT-US

TELEPHONE: (212) 977-9550

TELEFAX: (212) 644-6255

TELEFAX: (212) 646-625

TELEFAX: (212) 640-625

TELEFAX: (2
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; Patent No. 5750390
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: GENE
TITLE OF INVENTION: GENE
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
STREET: 611 West Sixth Street
CITY: Los Angeles
CITY: Los Angeles
CONTENTION: CENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
COUNTRY:
USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
"MRDIUM TYPE: 1EM Compatible
"MRUTER: IBM Compatible"
"V<TEM: IBM P.C. DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGCGTATCTGACAAG 15
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Matches 13; Conserva
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US-07-852-260-4
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US-07-936-421-18
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| CURRENT APPLICATION DATA:
| APPLICATION DATA:
| APPLICATION DATA:
| APPLICATION DATA:
| PILING DATE: 19920826
| CLASSIFTATION: 415
| PRIOR APPLICATION DATA: including application
| PRIOR APPLICATION DATA: described below:
| PRIOR APPLICATION DATA: described below:
| PRIOR APPLICATION DATA: described below:
| PILING DATE: 19970826
| PILING
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; ORGANISM: Homo sapiens
US-11-083-784-277064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-083-784-277064
Published Applications NA Main:*

1: FEMC Celerra SIDS3/ptodata/2/pubpna/USO7 PUBCOMB.seq:*
2: /EMC Celerra SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
3: /EMC_Celerra SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
4: /EMC_Celerra SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
5: /EMC_Celerra SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
6: /EMC_Celerra SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
7: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
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9: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
10: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
11: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
12: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
13: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
14: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
14: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
14: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
15: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIIIC_PUBCOMB.seq:*
16: /EMC_Celerra SIDS3/ptodata/2/pubpna/USIIC_PUBCOMB.seq:*
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Sequence 1347779,
Sequence 1348138,
Sequence 1368138,
Sequence 252899,
Sequence 880853,
Sequence 880853,
Sequence 880853,
Sequence 252899,
Sequence 1324693,
Sequence 1324691,
Sequence 346041,
Sequence 346141,
Sequence 346141,
                                                                                          June 9, 2006, 00:20:20; Search time 848 Seconds (without alignments) 304.293 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-083-784-277064
US-11-10-244-277064
US-10-310-914A-1347779
US-10-310-914A-1368338
US-11-083-784-252899
US-11-083-784-880853
US-11-083-784-1324693
US-11-101-244-880855
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-880956
US-11-101-244-346041
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          18892170 segs, 6143817638 residues
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                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   - nucleic search, using sw model
                                                                                                                                                                                   1 ctggcgtatctgaagagtctg 21
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Gapop 10.0 , Gapext 1.0
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Match Length DB
                                                                                                                                                      US-09-743-825-8
21
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Maximum DB seq length: 21
                                                                                                                                                      Title:
Perfect score:
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                                                                   nucleic
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                                                                                                                                                                                   Sequence:
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                                                                                              Run on:
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1330360, 252928, 252928, 1368384,

Sequence 2 Sequence 2 Sequence 1

Sequence Sequence

US-10-310-914A-566703

1410057

Sequence 1 Sequence 1 Sequence 3

Sequence

1227779,

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

276438, 276470, 277078, 366530, 825591, 825606,

Sequence Sequence

US-10-310-914A-1058239 US-11-083-784-276438 US-11-083-784-276470 US-11-083-784-36530 US-11-083-784-825501 US-11-083-784-825501 US-11-083-784-1002832 US-11-083-784-1002832 US-11-083-784-1002832 US-11-083-784-1410057 US-11-101-244-276438 US-11-101-244-276438 US-11-101-244-276438 US-11-101-244-1002932 US-11-101-244-1002932 US-11-101-244-1002932 US-11-101-244-110057 US-11-101-244-110057 US-11-101-244-110057 US-11-101-244-110057 US-11-101-244-110057 US-11-101-244-110057 US-11-101-244-11057 US-11-101-244-110057 US-11-101-244-110057 US-11-101-244-110057 US-11-013-114A-376212 US-11-013-114A-376212 US-11-013-144-1356384 US-11-01-244-1356384

Sequence Sequence Sequence

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                                                                                                                                               APPLICANT: Characton, Inc.
APPLICANT: Khovova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 277064
LEMEGRIF: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 14;
Pred. No. 5.1e+03;
; Mismatches 1;
ALIGNMENTS
                                                                                               ; Sequence 277064, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.6%;
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Best Local Similarity 68.8
Matches 11, Conservative
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US-11-101-244-277064

Sequence 1019, Ap

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Gaps
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Pred. No. 6.5e+03;
6; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                       Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Resynolds, Esphen
APPLICANT: Restinge, Stephen
APPLICANT: Restinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dharmacon, Inc.
APPLICANT: Chrorova, Ansatasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
                                                                                                                                                                                                                                                                                  Score 14.2; DB 11;
Pred. No. 6.5e+03;
0; Mismatches 3;
  CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFWARE: Patentin version 3.3 SEQ ID NO 1368338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 880853, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-083-784-252899
; Sequence 252899, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US/10/714,333
                                                                                                                                                                                                                                                                                                                                                                                              3 GGCGTATCTGAAGAGTCTG 21
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.6%;
52.6%;
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Best Local Similarity 52.6<sup>1</sup>
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-083-784-252899
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                           US-10-310-914A-1368338
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                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Publication No. US20060003322A1
Reblication No. US2006000332A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.CPUS01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.6%; Score 14.4; DB 11; Length 20; 93.8%; Pred. No. 5.1e+03; ive 0; Mismatches 1; Indels
                                                                          APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 00/502,050
FRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLILNG DATE: 2003-09-10
PRIOR PILLNG DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO S: 277064
LENGTH: 19
Sequence 277064, Application US/11101244
Publication No. US20050246794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGGCGTATCTGAAGA 16
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Best Local Similarity 68.88
Matches 11; Conservative
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Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-277064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-310-914A-1347779/c
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US-10-310-914A-1368338/c
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LENGTH: 20
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
NUMBER: OF SEQ ID NOS: 1591911
SEQ ID NO 1324693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 880853, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 252899, Application US/11101244
Publication No. US20050246794A1
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Best Local Similarity 52.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1324693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-101-244-252899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 880.56, Application US/11083784
; Bequence 880.56, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INPORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Arachall, William
; APPLICANT: Beake, Devin
; APPLICANT: Arachall, William
; APPLICANT: Arachall, William
; APPLICANT: Arachall, William
; PRICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REPERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR PLING DATE: 2003-11-14
; PRIOR PLING DATE: 2003-11-14
; PRIOR PLING DATE: 2003-11-14
; PRIOR PLING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 880956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1324693, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.; APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                Indels
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3;
                                                                                                                                                                                                                                                                                               Score 14.2; DB 14;
Pred. No. 6.5e+03;
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Best Local Similarity 57.9%; Pred. No. 6.5e
Matches 11; Conservative 5; Mismatches
PRIOR FILING DATE: 2003-11-14
PRIOR PLING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-880853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-083-784-880956
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       Length 19;
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Anastasia
APPLICANT: Marshall, William
APPLICANT: Marshall, William
FILE REFERENCE: 134990s
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11.14
SOFTWARE: Proprietary
SEQ ID NO S: 1591911
SOFTWARE: Proprietary
                                                Indels
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional siRNA
Score 14.2; DB 14;
Pred. No. 6.5e+03;
6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.6%; Score 14.2; DB 15;
Best Local Similarity 52.6%; Pred. No. 6.5e+03;
Matches 10; Conservative 6; Mismatches 3;
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Query Match
Best Local Similarity 52.6'
Matches 10; Conservative
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                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1324693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-11-083-784-346041
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Best Local Similarity
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US-11-083-784-346141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION

APPLICANT: Dharmacon, Inc.
APPLICANT: Rhvorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Devin
APPLICANT: Responds, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 880956
LENGTH: 19
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; Sequence 1324693, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Rivorova, Anastasia
; APPLICANT: Reake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Arehall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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             CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR PILING DATE: 2002-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 880956, Application US/11101244
Publication No. US20050246794A1
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1 UGAUGAAUCUGAAGAGUCU 19
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                                                                                                                                                                                                                                     ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-880853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-880956
FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Pred. No. 6.5e+03;
6; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.8; DB 14; Length 19;
Pred. No. 1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | GENERAL INVENTATION:
| GENERAL INVENTATION:
| APPLICANT: Characon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Leake, Devin
| APPLICANT: Barelal; William
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA
| TITLE OF INVENTION: Functional and Hyperfunctional
| FILE REPRENCE: 13499US
| CURRENT APPLICATION NUMBER: US/11/083,784
| PRIOR PILING DATE: 2003-11-14
| PRIOR PILING DATE: 2003-11-14
| PRIOR PILING DATE: 2003-11-14
| PRIOR PILING DATE: 2003-10-104
| PRIOR PILING DATE: 2002-11-14
| PRIOR FILING DATE: 2002-11-14
| SOFTWARE: Proprietary
| SEQ ID NO 346041
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Publication No. US2005024547541

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Marke, Devin

APPLICANT: Markell, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR PLILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 346041, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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1 UUGAGUAUCUGAAGAGU 17
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52.6%;
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65.7%; Score 13.8; DB 14; Length 19;
Best Local Similarity 58.8%; Pred. No. 1e+04;
Matches 10; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.7%; Score 13.8; DB 15; Length 19; Best Local Similarity 58.8%; Pred. No. 1e+04; Matches 10; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 346041, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Elake, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respending, Angela
APPLICANT: Respending, Angela
APPLICANT: Respending, Milliam
APPLICANT: Respending, William
APPLICANT: Marchall, William
APPLICANT: Leake, Devin
FILE REPERRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-00-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
SOUTHARE: Proprietary
SOUTHARE: Proprietary
SOUTHARE: Proprietary
SEQ ID NO 346041
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 346141
LENGTH: 19
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1 UUGAGUAUCUGAAGAGU 17
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                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-346141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-346041
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715, App 1168, Ap 2052, Ap 35, Appl

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US-10-994-215-56

US-10-994-215-56

Sequence 56, Application US/10994215

Publication No. US2006011302A1

GENERAL INFORMATION:

APPLICANT: The Scripps Research Institute

TILE OF INVERTION: COMPOSITIONS AND METHODS TO REDUCE MUTAGENESIS

TILE REFERENCE: 91-0001100S

CURRENT APPLICATION NUMBER: US/10/994,215

CURRENT FILING DATE: 2004-11-19

NUMBER OF SEQ ID NOS: 74

SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.8; DB 6;
Pred. No. 6.8e+02;
); Mismatches 2;
US-11-267-942-15
US-11-291-697-5255
US-11-291-697-613
US-11-251-465-770
US-11-235-385-7
US-11-235-385-21
US-11-235-385-21
US-11-235-385-35
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-173-889-66
US-11-242-111-69
US-11-242-111-69
US-10-511-937-2052
US-10-511-837-2052
US-10-511-837-355
US-11-336-198-4
US-11-336-198-4
US-11-336-198-4
US-11-336-198-4
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FUBLICATION No. US20060094008A1
GENERAL INFORMATION:
TITLE OF INVENTION: CK primer
FILE REFERENCE: GP03-1006F07
CURRENT PELING DATE: 2004-11-19
FRIOR PELICATION NUMBER: UF P2002-145689
FRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: UF P2002-175271
PRIOR APPLICATION NUMBER: UF P2002-175271
PRIOR PILING DATE: 2002-06-17
FRIOR PILING DATE: 2002-06-17
FRIOR FILING DATE: 2002-07-09
SOFTWARE: PARENTING DATE: 2002-07-09
SOFTWARE: PARENTING DATE: 2002-07-09
SOFTWARE: PARENTING DATE: 2002-07-09
SOFTWARE: PARENTING DATE: 2002-07-09
FRIOR FILING DATE: 2002-07-09
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1 Similarity 86.7%;
13; Conservative (
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     ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
  US-10-514-776-361
  TYPE: DNA
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10, Appl
5436, Ap
2, Appli
5003, Ap
587, App
2085, Ap
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Sequence
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                         GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-994-215-56

US-10-511-815-58

US-11-251-465-460

US-11-251-465-460

US-11-251-465-503

US-11-251-465-503

US-11-251-465-503

US-11-251-465-503

US-11-251-465-240

US-11-251-465-240

US-11-251-465-240

US-11-251-465-503

US-11-293-697-5003

US-11-293-697-5003

US-11-293-697-5003

US-11-293-697-5003

US-11-293-697-5003

US-11-204-427-36

US-11-204-427-36

US-11-251-465-588

US-11-251-465-588

US-11-251-465-588
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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21
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Maximum DB seq length: 21
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Gaps

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11.8 10.8 10.2 10.2 10.2 10 10 10 10 10 10 10

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Sequence 460, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys. Reginald
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
ITILE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify 7
ITILE OF INVENTION: Inflammatory Diseases
ITILE APPLICANT: Same, Useful In The Treatment Of Joint Degenerative And
ITILE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT PILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR APPLICATION DATE: 2005-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 277, Application US/11158209

Sequence 277, Application No. US2006008852A1

GENERAL INFORMATION:

APPLICANT: Dirk Petersohn

APPLICANT: Thomas Gassenmeier

APPLICANT: Thomas Gassenmeier

APPLICANT: Thomas Gassenmeier

APPLICANT: Marcus Conradt

FILING APPLICANT: Marcus Conradt

FRIOR FILING DATE: 2003-12-12

FRIOR FILING DATE: 2002-12-20

MUMBER OF SEQ ID NOS: 1335

SEQ ID NO 277

FROWTHAL: SEQUENCE CONTRACT

FROWTHAL: APPLICANT OF A
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47.6%; Score 10; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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48.6%; Score 10.2; DB 7;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 12; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 880
SOFWARE: Patentin version 3.3
SEQ ID NO 460
LENGTH: 21
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                     3 GGCGTATCTGAAGAG 17
                                                                                   7 GGCGAAACTGAAGTG 21
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; ORGANISM: Homo Sapiens
US-11-158-209-277
                                                                                                                                                                                            RESULT 5
US-11-251-465-460/c
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Sequence 22, Application US/10539032

Sequence 22, Application US/10539032

Sequence 22, Application US/10539032

GENERAL INFORMATION:

APPLICANT: JAPAN SCIENCE AND TECHNOLOGY AGENCY

TITLE OF INVENTION:

GURRENT APPLICATION NUMBER: US/10/539,032

CURRENT APPLICATION NUMBER: US/10/539,032

CURRENT APPLICATION NUMBER: US/10/539,032

FRIOR PILING DATE: 2005-06-13

FRIOR PILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 30

SSOFTWARE: Patentin Ver. 2.1

LENGTH: 21
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** OTHER INFORMATION: Description of Artificial Sequence:NaGLT1 reverse;

** OTHER INFORMATION: primer
US-10-539-032-22
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Publication No. US20060105973A1

GENERAL INFORMATION:

APPLICANT: SUBJANT NUMBER INFORMATION:

TITLE OF INVENTION: 11-BETA DEHYDROGENASE I EXPRESSION

FILE REPERBURE: RTS-0428

CURRENT APPLICATION NUMBER: US/10/511,832

CURRENT PILING DATE: 2004-10-19

NUMBER OF SEQ ID NOS: 122

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20
                                                                                                                                                                                                                                                  Query Match 51.4%; Score 10.8; DB 6; Length 19; Best Local Similarity 85.7%; Pred. No. 2.3e+03; Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.6%; Score 10.2; DB 6; Length 20; Best Local Similarity 80.0%; Pred. No. 4.8e+03; Matches 12; Conservative 0; Mismatches 3; Indels
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; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; PERTURE:
; OTHER INFORMATION: synthetic oligonucleotide primer US-10-994-215-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-511-832-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0
Matches 12; Conservative
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APPLICANT: TUMBS, Daniel
APPLICANT: TOWAS, MAISTANEM APPLICANT: TOWAS, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: DATIE ROCDING THE SAME
FILE REFERENCE: P2548PIC.
CURRENT APPLICATION NUMBER: US/09/866,028
PRIOR PILING DATE: 2005-12-07
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 06/069,334
PRIOR PILING DATE: December 3, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PLING DATE: December 16, 1997
PRIOR PLING DATE: DECEMBER 17, 1997
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                                                                                                                                                   Sequence 106, Application US/11296092
Publication No. US20060105427A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 240, Application US/11251465; Publication No. US20060094061A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TGGCGTATCTGAAGAGTC 19
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                 Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                               Filvaroff, Bllen
                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                    Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurney, Austin
Hillan, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Napier, Mary
Roy, Margaret
Tumas, Daniel
               3 GAAGAGTCTG 12
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                                                                                                                                                                                                                                                                                                   Baton, Dan
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                                                                                                                           US-11-296-092-106
                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                            Sequence 137, Application US/11251465

Sequence 137, Application No. US20060094061A1

SERREAL INPORMATION:
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
APPLICANT: Tomme, Peter
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: 101/2-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT APPLICATION NUMBER: 60/619,384
PRIOR PILIAG DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE PATEURIN VERSION 3.3
SEQ ID NO 137
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 503, Application US/11251465

Publication No. US20060094061A1

GENERAL INFORMATION:

APPLICANT: Brys, Reginald

APPLICANT: Tomme, Peter

APPLICANT: Tomme, Peter

APPLICANT: Tasassen, Hubertus

TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Same, USeful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Same, USeful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION NUMBER: 06/11/251,465

CURRENT APPLICATION NUMBER: 06/19,384

PRIOR FILING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 880

SOUTHWARE: Patentin version 3.3

SEQ ID NO 503

LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Knock-down target sequence US-11-251-465-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Knock-down target sequence US-11-251-465-503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 10; Conservative
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Matches 10; Conservative
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10 CTGAAGAGTC 1
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APPLICANT: Albig, Allan R.
TITLE OF INVENTION: Fibulin-3 and Uses Thereof;
FILE REFERENCE: 2879-109
CURRENT APPLICATION NUMBER: US/11/267,942
CURRENT FILING DATE: 2005-11-04
PRIOR APPLICATION NUMBER: 60/625,598
PRIOR APPLICATION NUMBER: 60/627,129
PRIOR PILING DATE: 2006-03
PRIOR FILING DATE: 2005-06-03
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 10
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGCGTATCTGAAGAGTCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GGCATATCCACAGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: primer US-11-267-942-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: primer US-11-264-029-10
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial
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Sequence 504, Application US/11251465

Bublication No. US20060094061A1

Sequence 504, Application US/11251465

Hublication No. US20060094061A1

APPLICANT: Wandeghinate, Nick

APPLICANT: Vandeghinate, Nick

APPLICANT: Tomme, Peter

TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Dome, Useful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: NUMBER: US/11/251,465

CURRENT APPLICATION NUMBER: US/11/251,465

CURRENT APPLICATION NUMBER: 60/619,384

PRIOR APPLICATION NUMBER: 60/619,384

PRIOR APPLICATION NUMBER: 2004-10-15

NUMBER OF SEQ ID NOS: 880

SOFTWARE PatentIn Version 3.3

LENGTH: 21
                                                                                        TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
FILE REFERENCE: P30,172-A US
CURRENT PILING DATE: 2005-10-14
PRIOR PAPLICATION NUMBER: 60/619,384
PRIOR PILING DATE: 2005-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: Patentin version 3.3
SEQ ID NO 2.40
LENGTH: 21
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47.6%; Score 10; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 10; Conservative 0; Mismatches 0;
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                       Vandeghinste, Nick
Tomme, Peter
Klaassen, Hubertus
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Brys, Reginald
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                                                 APPLICANT:
APPLICANT:
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Query Match 47.6%; Score 10; DB 7; Length 21; Best Local Similarity 72.2%; Pred. No. 6.2e+03; Matches 13; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                  Sequence 10, Application US/11264029
Publication No. US20060099171A1
GENERAL INFORMATION:
APPLICANT: University of Pennsylvania
TITLE OF INVENTION: MCITRL IS COSTIMULATORY FOR T CELLS
FILER REFREENCE: P-8296-US
CURRENT APPLICATION UNMBER: US/11/264,029
CURRENT APPLICATION UNMBER: 2005-11-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.3
SEQ ID NO 10
LENGTH: 21
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Sequence 5436, Application US/11293697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA

FILE REPERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT PILING DATE: 2005-12-05

PRIOR PRIOR PILING DATE: 2002-13-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5436

LENGTH: 18
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RESULT 12
US-11-267-942-10/c
; Sequence 10, Application US/11267942
; Publication No. US20060094054A1
; GENERAL INFORMATION:
; APPLICANT: Schiemann, William P.

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Sequence 2, Application US/11283484A

Sequence 2, Application US/11283484A

Publication No. US20060115461A1

GENERAL INFORMATION:

APPLICANT: Bobarmacon, Inc.

APPLICANT: Robinson, Rathryn

APPLICANT: Marshall, William S.

APPLICANT: Marshall, William S.

APPLICANT: Marshall, William S.

APPLICANT: Marshall, William S.

APPLICANT: APPLICANT: Mober No. 16542.1

CURRENT APPLICATION NUMBER: US/11/283,484A

CURRENT FILING DATE: 2005-11-18

PRIOR PILING DATE: 2005-11-22

PRIOR APPLICATION NUMBER: 60/630320

PRIOR PILING DATE: 2005-04

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.3

SEQ ID NO 2

TYPE: DNA

PRAWTHER: Homo sapiens

    TYPE: DNA
    ORGANISM: Artificial Sequence
    FRATURE:
    OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized
    US-11-293-697-5436

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                                                                                                                                               Query Match

46.7%; Score 9.8; DB 7; Length 18;
Best Local Similarity 84.6%; Pred. No. 7.78+03;
Matches 11; Conservative 0; Mismatches 2; Indels
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46.7%; Score 9.8; DB 7; Length 19;
Best Local Similarity 84.6%; Pred. No. 7.7e+03;
Matches 11; Conservative 0; Mismatches 2; Indels
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FRATURE:
NAME/KEY: mlsc_feature
COTATION: (11...(19)
US-11-283-484A-2
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US-11-283-484A-2
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Search completed: June 9, 2006, 00:36:32 Job time : 25 secs

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Title: Perfect score:

Sequence:

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Scoring table:

Searched:

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AX207008 Sequence
AX333519 Sequence
CS005340 Sequence
IG1735 Sequence 28
AX66529 Sequence
AX1364674 Sequence
AX74698 Sequence
AX74698 Sequence
AX71910 Sequence
AX130020 Sequence
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AX130020 Sequence
AX130020 Sequence
AX20915 Sequence
AX20943 Sequence
AX20943 Sequence
AX20943 Sequence
AX20943 Sequence
AX378663 Sequence
AX378663 Sequence
AX378663 Sequence
AX13092 Sequence
CQ889993 Sequence
CQ889993 Sequence
CQ889993 Sequence
CQ889993 Sequence
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I (bases I to 20)

Griffan, R. Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 2812 06-MAY-2003;
Genset, S.A.;;
FRX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 1e+04; ive 0; Mismatches 2; Indels
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Sequence 2812 from patent US 6559294.
AR312275
AR312275.1 GI:31705701
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Sequence 48 from patent US 6828151.
AR614263.1 GI:56670377
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1. .20
/organism="unknown"
/mol_type="genomic DNA"
CS015023
AX207008
AX207008
AX353119
CS005340
CS005340
AX1313092
AX131002
AX131002
AX270943
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Best Local Similarity 88.2
Matches 15; Conservative
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AR312275
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AR614263 Sequence
AR6134611 Sequence
AR05464 Sequence
BD217452 Antisense
AR031072 Sequence
AR011072 Sequence
AR152833 Sequence
AR152833 Sequence
AR75344 Sequence
AR75345 Sequence
AR75346 Sequence
AR75306 Sequence
AR75307 Sequence
AR048183 Sequence
BL0136 PCR primer
DD200317 RNA Inter
DD200317 RNA Inter
DD200470 RNA Inter
AR033697 Sequence
CS014609 Sequence
                                                                                        9, 2006, 00:36:46 ; Search time 1983 Seconds (without alignments) 644.956 Million cell updates/sec
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          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    6366136 segs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                nucleic search, using sw model
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AR614263
AR614263
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AR096404
BD217452
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AR152833
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AR163834
AR718344
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AR7183434
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Gapop 10.0 , Gapext 1.0
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2: gb_pat: *
3: gb_ph: *
5: gb_ph: *
6: gb_pr: *
6: gb_pr: *
7: gb_er: *
7: gb_
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PAT 12-JUN-2003

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PAT 15-DEC-2004

linear

DNA

Unknown. Unknown.

DD200470 AR023697 CS014609

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PN JF 200219015-A/75
PN JF 200219015-A/75
PP 17-JUN-1999 JP 2000557265
PR 26-JUN-1999 US 09/106038
PI BRENDA F BAKER, LEX M COWSERT
PC C12N15/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC C12N15/09, A61K31/7105, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC C12N15/09, A61K31/711, A61K48/00, A61P29/00, A61P43/00, PC C12N15/09, Linear;
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of TNFR1 expression
FH Rey Location/Qualifiers
FT SOURCE 1. 18
FT FOURTH PARTIES AND COMPANY PROGRAMMENT PARTIES AND COMPANY PARTIES AND CO
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Redery, J.N., Schatzman, R.C. and Tsuchihashi, Z.
Redery, J.N., Schatzman, R.C. and Tsuchihashi, Z.
Methods and compositions for diagnosis and treatment of iron
misregulation diseases
Patent: US 6849399-A 11 01-FEB-2005;
Bio-Rad Laboratories, Inc.; Hercules, CA
Location/Qualifiers
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       Length 18;
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    61.0%; Score 12.2; DB 2; Length 1
82.4%; Pred. No. 8.3e+04;
ive 0; Mismatches 3; Indels
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BD217452.
JP 2002519015-A/75.
unidentified
unidentified
unidassified sequences.
Ubases 1 to 18)
Baker, B.F. and Cowsert, L.M.
Antisense modulation of TWFR1 expression
Patent: JP 2002519015-A 75 02-JUL-2002;
ISIS PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                        BD217452 18 bp DNA
Antisense modulation of TNFR1 expression.
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Sequence 11 from patent US 6849399.
AR633610
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/organism="unidentified"
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/db_xref="taxon:32644"
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                        Best Local Similarity
Matches 14; Conserv
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BD217452/c
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AUTHORS
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JOURNAL
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AR633610
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                 1 (bases 1 to 20)
Borchers, A.H. and Dobie, K.W.
Antisense modulation of hematopoietic cell protein tyrosine kinase expression
Patent: US 6828151-A 48 07-DEC-2004;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM Unknown.
Unclassified.
Unclassified.
SE 1 (bases 1 to 20)
RS Peder,J.N., Schatzman,R.C. and Tsuchihashi,Z.
Amthods and compositions for diagnosis and treatment of iron misregulation diseases
NAL Patent: US 6849399-A 12 01-FEB-2005;
Bio-Rad Laboratories, Inc.; Hercules, CA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       Length 20;
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66.0%; Score 13.2; DB 2;
Best Local Similarity 83.3%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 3;
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Baker, B.F. and Cowsert, L.M.
Antisense inhibition of TNFRI expression
Patent: US 6007995-A 75 28-DEC-1999;
Location/Qualifiers
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AR633611
AR633611.1 GI:59783856
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AR096404
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                                                                                                                                                                                          1. .20
/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
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Best Local Similarity 78.9
Matches 15; Conservative
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AR633611
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sequences involved in phenomena of tumour suppression, tumour reversation, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 934 27-MAR-2003;
Molecular Engines Laboratories (FR)
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                                                                                                                                          other sequences, artificial sequences.

1 (bases 1 to 20)

Sidlanski, D.

Detection of neoplasia by analysis of saliva

Patent: JP 2002505888-A 113 26-FEB-2002;

THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS TALIficial Sequence
PN JP 2002505888-A/113
PN 20-PEB-2002
PP 10-MAR-1999 JP 2000535774
PR 10-MAR-1998 US 09/038637
PR 10-MAR-1998 US 09/038637
PC CLUSINS/09,CL2Q1/68,CL2N15/00
CC nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.0%; Score 12; DB 2; Length 20; Best Local Similarity 75.0%; Pred. No. 1.1e+05; Matches 15; Conservative 0; Mismatches 5; Indels
                                    linear
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                         Detection of neoplasia by analysis of saliva.
BD134289 1 G1:23229234
JP 2002505888-A/13.
SYnthetic construct
Synthetic construct
contract
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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AX735344.1 GI:30514621
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Polymeropoulos,M.H. and Merril,C.R.
Eleven highly informative microsatelite repeat polymorphic DNA
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Pred. No. 1.1e+05;
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Sequence 60 from patent US 5861504.
AR031072 AR031072.1 GI:5944286
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/wol_type="unassigned DNA"
1. .20
/organism="unknown"
/mol_type="genomic DNA"
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1 (bases 1 to 18)

Komai,K., Kaneko,H. and Nakatsuka,I.
Oligonuclectide for use in checking presence or absence of mutation in human-derived cytochrome P450IIC18 gene
Patent: US 5821062-A 1 13-0CT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 18)
CIGAGNOLESCATE AND NAKATSUKA, I.
CIGONUCLECOTIDE FOR AMPLIFYING MUTATION TYPE GENE OF HUMAN DERIVED
CYTOCHROME P45-0118
PATENT: JP 1995285987-A 1 31-OCT-1995;
SUMITOMO CHEM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 bp DNA linear PAT 29-SEI
PCR primer to amplify mutated genes encoding human cytochrome
P450IIC18.
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86.7%; Pred. No. 1.4e+05;
ive 0; Mismatches 2;
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/organism="unknown"
/mol_type="unassigned DNA"
           Sequence 1 from patent US 5821062.
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/organism="unidentified"
/mol_type="genomic DNA"
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Artificial sequences.
JP 1995285987-A/1
31-0CT-1995
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E10136.1 GI:22026764
JP 1995285987-A/1.
unidentified
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF PATENT: WO 9735973-A 8 02-OCT-1997;
VETIGEN (FR)
Other publication FR 2746813 19971003.
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Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
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Sequence 2386 from Patent WO03040369.
AX759065
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 8 from Patent W09735973.
A65727
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L Patent: JP 2005517423-A 26 16-JUN-2005;
Sirna Therapeutics Inc
OS Artificial Sequence
PA Artificial Sequence
PN JP 2005517423-A/26
PD 16-JUN-2005
PR 11-FEB-2003 JP 2003569157
PR 06-JUN-2002 US 66/440129; 12-NOV-2002 US 66/4358580, PR 15-JAN-2003 US 66/440129; 12-NOV-2002 US 66/440124; PR 29-A0C-2002 US 66/406784, 05-SEP-2002 US 66/408378 PI leonid beigelman, james mcswiggen CC Description of Artificial Sequence: Target Sequence/siNA CC Bense region
                                           DD200317
RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta Receptor Gene Expression Using Short Interfering Nucleic Acid
                                                                                                              DD200317.1 GT:85651394
DD200317.1 GT:85651394
JP 2005517423-A/26.
SYnthetic construct
Synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 19)
Beigelman, L. and Mcswiggen, J.
RNA Interference Mediated Inhibition of TGF-Beta Receptor Gene Expression Using Short Interfering Nucleic Acid (siNA)
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    .19
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/db_xref="taxon:32630"

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9         45.0         20         14         AGI88131         AGI88131         Pan trog1           8.8         44.0         13         13         CZ172217         MIAA-3C07           8.8         44.0         13         13         CZ175846         CZ172817         MIAA-17K2           8.8         44.0         13         13         CZ175917         CZ175976         MIAA-1810           8.8         44.0         14         13         CZ172210         CZ172210         MIAA-1623           8.8         44.0         14         13         CZ172210         CZ172210         MIAA-3C23           8.8         44.0         14         13         CZ172210         CZ172210         MIAA-3C23           8.8         44.0         14         13         CZ172230         CZ172210         MIAA-3C23           8.8         44.0         14         13         CZ173186         CZ172210         MIAA-3C23           8.8         44.0         14         13         CZ17348         MIAA-2C30           8.8         44.0         14         13         CZ17503         MIAA-1N2           8.8         44.0         14         13         CZ17503         MIAA-1N	ALIGNMENTS  CO792214  19 bp mRNA linear EST 05-AUG-2004 NT014C A10 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5' similar to hypothetical protein, mRNA sequence. CO792214.1 G1:51008185 EST. Ambystoma mexicanum (axolot1) Ambystoma mexicanum (axolot1) Ambystoma mexicanum (axolot1) Ambystoma mexicanum (axolot1) Ambystoma (axolot1) Ambystoma (axolot1) Ambystoma (axolot1) Ambystoma. I (bases 1 to 19) Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K., Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M. Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M. expressed sequence tags from embryonic and regenerating blastema	
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n 5.1.9  Biocceleration Ltd.  Biocceleration Ltd.  earch time 2496 Seconds (without alignments)  448.072 Million cell updates/sec  residues  meters: 14588	cted by chance to have a soft the result being printed, score distribution.	Description  C0792214 NT014C_A1  C2172219 MIAA_3G17  C2174095 MIAA_25J1  C2174095 MIAA_21H0  C2174095 MIAA_21H0  C217508 MIAA_21H0  C2175608 MIAA_3D23  C2176205 MIAA_3D23  AJ840659 Arabidops  AZ309643 IMO16E23  CZ17781 MIAA_3H13  CZ17236 MIAA_3H13  CZ17236 MIAA_3H13  CZ17236 MIAA_3H13  CZ17231 MIAA_3H13  CZ17231 MIAA_3H13  CZ17231 MIAA_3H13  CZ17231 MIAA_3H13  CZ17231 MIAA_3H13  CZ17231 MIAA_3H13  CZ17831 MIAA_5H19  AJ671616 AJ671616
GenCore version 5.1.9  Copyright (c) 1993 - 2006 Bioccele OM nucleic - nucleic search, using sw model Run on: June 9, 2006, 00:41:53; Search time (without a 448.072 Mi Title: US-09-743-825-10 Sequence: 1 gaccgcatagactcccaga 20 Sequence: 1 gaccgcatagactcccaga 20 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 48236798 seqs, 27959665780 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 20 Post-processing: Minimum Match 0% Maximum Match 100%	stl:* tt4:* tt4:* tt5:* tt5:* tt6:* tt7:* stl:*	Result Query No. Score March Length DB ID  1 10.2 51.0 19 8 CO792214 2 9.8 49.0 14 13 CZ17219 3 9.8 49.0 14 13 CZ174095 4 9.8 49.0 14 13 CZ174095 6 9.8 49.0 14 13 CZ174508 7 9.8 49.0 14 13 CZ174508 7 9.8 49.0 14 13 CZ176208 9 9.8 49.0 14 13 CZ176208 10 9.8 49.0 14 13 CZ176208 11 9.8 49.0 14 13 CZ176208 12 9.8 49.0 14 13 CZ176208 13 9.6 48.0 20 11 AZ660128 14 9.2 46.0 15 13 CZ17236 15 9.2 46.0 17 13 CZ178189 1 9 45.0 19 1 AZ671616 1 9 45.0 19 13 CZ17780

Query Match

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RESULT 2 CZ172219

ACCESSION VERSION KEYWORDS SOURCE ORGANISM JOURNAL

TITLE

FEATURES

REFERENCE AUTHORS

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(MIAAGSS 001)"
                                                                                                                                          Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
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Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Mylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Mitreva,M., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
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                                                                                            Meloidogyne incognita (southern root-knot nematode)
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84.6%; Pred. No. 3.3e+06;
ative 0; Mismatches 2;
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                                           CZ174095.1 GI:58342388
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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Unpublished Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
NotI-SalI site of pCMVSport6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 kB.
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Pred. No. 3.3e+06;
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Meloidogyne incognita
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strain="Race 1"
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RESULT 3 CZ174095 LOCUS DEFINITION

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/db_xref="taxon:6306"
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Meloidogyne incognita
Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
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Meloidogyne incognita
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylencholdea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: nemacode@watson.wustl.edu
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/mol_type="genomic DNA"
/strain="Race 1"
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                   11; Conservative
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(MIAAGS 001)
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Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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BAC ends sequenced by Washington University Genome Sequencing Center Class: BAC ends.

Location/Qualifiers
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BAC ends sequenced by Washington University Genome Sequencing
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Unpublished (2005)
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Washington University in St. Louis
Washington University School of Medicine
444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, 14 71: 314 286 1810
Pax: 314 286 1810
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/organism="Meloidogyne incognita"
/organism="genemic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
/dev_stage="L2"
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Pred. No. 3.3e+06;
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/clone_lib="Melc
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/dev_stage="L2"
/clone lib="Meloidogyne incognita BAC end sequence library
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| clone lib="Meloidogyne incognita BAC end sequence library
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Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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BAC ends sequenced by Washington University Genome Sequencing
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 3.3e+06;
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/strain="Race 1"
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CZ178035.1 GI:58346328
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Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
  1 (bases 1 to 14)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
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BAC ends sequenced by Washington University Genome Sequencing

    nematode@watson.wustl.edu
ends sequenced by Washington University Genome Sequencing

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Fel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
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Contact: Mirreva M
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Fal: 314 286 1800
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/organism="Meloidogyne incognita"
/mol type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"

    .14
/organism="Meloidogyne incognita"
/mol_type="genomic DNA"

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Pred. No. 3.3e+06;
0; Mismatches 2;
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Location/Qualifiers
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| Similarity 84.6%;
| 11; Conservative
                                                                                             incognita
Unpublished (2005)
Contact: Mitreva M
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Best Local Similarity 84.6
Matches 11; Conservative
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(MIAAGSS 001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-SEP-2004) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Bry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (Inttp://www.genoplante.com and http://genoplante-info.info.iopiogen.fr).

Location/Qualifiers
                                                 AJ840659 18 bp DNA linear GSS 08-FEB-2006
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
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                                                                                                                                                                                                                                                                                                                                   Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
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                                                                                                                                        AJ840659.1 GI:52544865
GSS; right border; T-DNA flanking sequence.
Arabidopsis thallana (thale cress)
Arabidopsis thallana
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    18
/note="T-DNA flanking sequence
right border"

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/cultivar="Wassillewskija"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
                                                                                                   genomic survey sequence.
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AZ309643.1 GI:10350661
GSS.
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Balzergue, S.
Direct Submission
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonacleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Meloidogyne incognita
Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
                                                                                                                                                                                                              Contect: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T., Reilly, M., Rose, M., Kose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Pred. No. 3.4e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0016 row: B column: 23
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 19.
Location/Qualifiers
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84.6%;
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/clone lib="Meloidogyne incognita BAC end sequence library
(MIAAGSS 001)"
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20 bp DNA linear GSS 14-DEC-200
1M0538G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                     1 (bases 1 to 20)
Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                            Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tal: 314 286 1800
Fax: 314 286 1810
Email: nematode@wastson.wustl.edu
Email: nematode@wastson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Meloidogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0538 row: G column: 04
Seg primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:6306"
                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends.
Location/Qualifiers
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AZ660128.1 GI:11797274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                        Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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AZ660128/c
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VERSION
KEYWORDS
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                     REFERENCE
                                              AUTHORS
                                                                                                                                        JOURNAL
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                                                                                          TITLE
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                                                                                                                                                                 COMMENT
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone l1b="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oilgonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil/4732114 gbl/APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Meloidogynidae, Meloidogyninae, Meloidogyne.
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,M., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MIAA-3X13c.g1 Meloidogyne incognita BAC end sequence library (MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
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Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                             organism="Mus musculus"
                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
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Fax: 314 286 1810
Email: nematode@watson.wustl.edu
                                                                                                                                                                                                                              db_xref="taxon:10090"
clone="UUGC1M0538G04"
High quality sequence stop: 20.
Location/Qualifiers
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Unpublished (2005)
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9, 2006, 01:56:22

Search completed: June Job time: 2498 secs

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/dev_stage="L2"

Clone lib="Meloidogyne incognita BAC end sequence library
(MIAAGSS 01)"

/note="Vector: pcUGI; Site_1: HindIII; Site_2: HindIII;
BAC library constructed by Arief Budiman and Nathan Lakey
at Orion Genomics, and David Bird and Charles Opperman at
Center for the Biology of Nematode Parasitism at NCSU."
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MIAA-3N19c.g1 Meloidogyne incognita BAC end sequence library
(MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
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/clone lib="Meloidogyne incognita BAC end sequence library
(MIAAGSS 001)"
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Meloidogyne incognita
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylencholdea; Meloidogynidae; Meloidogyninae; Meloidogyne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII; BAC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
Genome Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                                                                                                                                                                                                                Gaps
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BAC ends sequenced by Washington University Genome Sequencing
Center
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Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                            Score 9.2; DB 13; Length 15;
Pred. No. 7e+06;
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Pred. No. 7e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                           3; Indels
/organism="Meloidogyne incognita"
|mol_type="genomic DNA"
|strain="Race 1"
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/organism="Meloidogyne incognita"
/mol type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                 /db_xref="taxon:6306"
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Location/Qualifiers
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CZ178031.1 GI:58346324
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Matches 11; Conservative
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Matches 11; Conservative (
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COMMENT
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Sequence 289, App
Sequence 4, Appli
Sequence 4, Appli
Patent No. 5401629
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Sequence 113, Appl
Sequence 1, Appli
Sequence 8, Appli
Sequence 14, Appli
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Sequence 48, Appl
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Sequence 1239, Ap
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Sequence 20, Appl
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Sequence 4697, Ap
Sequence 113, App
                                                                                                                               June 9, 2006, 01:14:56 ; Search time 99 Seconds (without alignments) 378.002 Million cell updates/sec
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-696-791-1238
US-09-696-791-1239
US-08-974-180-35
US-10-148-806-20
US-10-148-806-21
US-09-422-978-4697
US-09-422-978-4697
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   1403666 seqs, 935554401 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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20
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                         Run on:
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13, App	04, App	6, Appl	744, Ap	204, App	B, Appl	2, Appl	29, App	2, Appl	29, App	, Appli	l. Appli	202, App	43, App	, Appli	7, Appl	99, App	340, Ap	2242, Ap	399, App	242. Ap	2242. Ap
Sequence 1	Sequence 2	Sequence 3	Sequence 3	Sequence 2	Sequence 2	Sequence 3	Sequence 6	Sequence 3	Sequence 6	Sequence 4	_	Sequence 2		u	m	Sequence 3	Sequence 5		Sequence 3	• • •	
US-08-256-426B-113	US-09-249-730-204	US-09-359-756-36	US-09-198-452A-3744	US-09-249-247-204	US-09-975-123-28	US-09-544-398B-32	US-09-544-398B-629	US-09-543-771B-32	US-09-543-771B-629	US-08-357-791-4	US-09-937-862B-1	US-09-081-646-202	US-09-081-646-743	US-09-124-398-5	US-09-659-791A-37	US-08-985-162-399	US-08-584-040-5340	US-09-371-772B-2242	US-09-401-063-399	US-09-685-664B-2242	US-10-138-674B-2242
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26.0	56.0	56.0 2	56.0	56.0 2	56.0 2	55.0	55.0	55.0	55.0	55.0 2	55.0 2	54.0 1	54.0 1	54.0 1	54.0 2	53.0	53.0	53.0	53.0	53.0	53.0
11.2	11.2	11.2	11.2	11.2	11.2	11	11	11	נו	11	11	10.8	10.8	10.8	10.8	10.6	10.6	10.6	10.6	10.6	10.6
24	22	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment_ITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: 003.999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 3;
Pred. No. 6.7e+02;
0; Mismatches 2;
RESULT 1
2.09-198-452A-2812
; Sequence 2812, Application US/09198452A
; Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACCGCATAGACTTCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GACCGCATAAACTTATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                       SEQ ID NO 2812
                                                                                                                                                                                                                                                                                                                                  LENGTH: 20
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RESULT 2
US-10-007-010-48/c
i Sequence 48, Application US/10007010
j Patent No. 6828151
j GENERAL INFORMATION:
i APPLICANT: Alexander H. Borchers
i APPLICANT: Alexander H. Bobie
j TILE ROF INVENTYON: ANTISENSE MODULATION OF HCK EXPRESSION
i TILE ROF INVENTY FILING DATE: 2001-12-04
j NUMBER OF SEQ ID NOS: 87
j SEQ ID NO 48
j LENGTH: 20
j TYPE: DNA
organism: Artificial Sequence
j FRATURE:
j CTHER INFORMATION: Antisense Oligonucleotide

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Sequence 75, Application US/09106038A
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                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Schatzman, Randall C.
APPLICANT: Tsuchihashi, Zenta
ITILE OF INVENTION: DEACHOSS AND COMPOSITIONS FOR
TITLE OF INVENTION: DEACHOSS AND TREATMENT OF IRON MISREGULATION D
TITLE OF INVENTION: ISEASES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                            Length 20;
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Pred. No. 2.9e+03;
0; Mismatches 4; Indels
                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUNTRY: NY
COUNTRY: NY
COUNTRY: NY
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
SOFTWARE: PARESEN WINDOWS VERSION 2.0b
APPLICATION NUMBER: US/08/920,559
FILING DATE: 27-AUG-1997
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 13-WAY-1996
APPLICATION NUMBER: US 08/66,211
FILING DATE: 13-UN-1997
RILING DATE: 13-UN-1997
RILING DATE: 13-UN-1997
RILING DATE: 13-UN-1997
APPLICATION NUMBER: US 08/866,211
REFERENCE/DOCKET NUMBER: 28,462
                                                    Query Match
66.0%; Score 13.2; DB 3;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08920559 Patent No. 6849399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACCGCATAGACTTCTCAG 19
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78.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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EDNESS: single
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Best Local Similarity
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US-09-106-038A-75/c
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TOPOLOGY:
US-08-920-559-12
US-10-007-010-48
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US-08-920-559-12
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APPLICANT: Schatzman, Randall C.
APPLICANT: Schatzman, Randall C.
APPLICANT: Tsuchihashi, Zenta
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF IRON MISREGULATION DIAGNOSIS AND TREATMENT OF IRON MISREGULATION DIMER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Parent No. 6007995
GENERAL INFORMATION:
APPLICANT: Brenda P. Baker and Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF THE TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
STREET: 2292 Faraday Avenue
CITY: Carlsbad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,559
                                                                                                                                                                                                                    CUITI: CACOUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION: 514
ATTORNEY/ABGNI INFORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37,280
REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (760) 931-9200
TELEFRAM: (760) 931-9200
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-920-559-11
; Sequence 11, Application US/08920559
; Patent No. 6849399
; GENERAL INFORMATION:
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COUNTY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CGCATAGACTTCTCAGA 20
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Best Local Similarity 82.4%;
Matches 14; Conservative
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-75
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Length 20;
                                                        Length 20;
                                                                                                                                                                                                                                                                                         Sequence 60, Application US/07799828C

Patent No. 5378602

GENERAL INFORMATION:

APPLICANT: Drs. Carl R. Merril and APPLICANT: Minael H. Polymeropoulos

TITLE OF INVENTION: MICROSATELLITE REPRAT

TITLE OF INVENTION: MICROSATELLITE REPRAT

TITLE OF INVENTION: POLYMORPHIC DNA MARKERS

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSER: Lowe, Price, LeBlanc & Becker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60, Application US/07952277A

Patent No. 5861504

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Dra. Mihael H. Polymeropoulos

APPLICANT: and Carl R. Merril

TITLE OF INVENTION: RELEVEN HIGHLY INFORMATIVE

TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.0%; Score 12; DB 2; Le
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 5;
                                                 60.0%; Score 12; DB 2; 75.0%; Pred. No. 6.1e+03; 1ve 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lowe, Price, LeBlanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/799,828C
                                                                                                                                                                                 1 GACCCCACAGCCTATTCAGA 20
                                                                                                                                             1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. MILLS
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 71701
TELECOMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACCGCATAGACTTCTCAGA 20
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                                                 Query Match
Best Local Similarity 75.0°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
STATE: Virginia
COUNTRY: USA
  US-07-922-723A-60
                                                                                                                                                                                                                                                        RESULT 7
US-07-799-828C-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.0%; Score 12.2; DB 3; Length 20; 82.4%; Pred. No. 4.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-07-922-723A-60

i Sequence 60, Application US/07922723A

i Patent No. 5369004

i GENERAL INFORMATION:

APPLICANT: Drs. Mihael H. Polymeropoulos

ITILE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS

TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSE: Lowe, Price, LeBlanc & Becker

STREET: Sulte 300, 99 Canal Center Plaza

STREET: Virginia

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                             8907-0062-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22314
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: DGS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/922,723A
                     CLASSIPICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/652,265
PILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/834,497
PILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/866,211
FILING DATE: 13-UNN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  ALICKAEL, POSSEART, BITAN MERICAL MAME: POISSEART, BITAN MERICAL BY 462 REFERENCE DOCKET NUMBER: 8907-TELEPHONE: 650-493-4935 TELEPHONE: 66141 PENNIE INFORMATION POR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs TYPE: nucleic acid STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.G. Mills
REGISTRATION NUMBER: 34506
REGISTRATION NUMBER: 71701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACCGCATAGACTTCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GACAGCACAGACTTCAC 18
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
27-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-920-559-11
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                  619/678-5099
                                                                                                                                                                                                                                     US-09-038-637-113
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US-08-716-459-1/c
                                                                TELEFAX:
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APPLICANT: SIGTANSKY, David
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,637
FILING DATE: 10-MAR-1998
PRIOR APPLICATION NUMBER: 08/579,233
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/152,313
FILING DATE: 12-NOV-1993
ATTORNEY AGENT TIPORMATION:
...urksSEE: Lowe, Price, LeBlanc & Becker STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia COUNTRY: USA ZID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOKNE, FALLE, LISA A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 07265/146001
                                                                                                                                                              ZIP: 22314
COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS TEXT File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,277A
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 717081C
TELECOMMUNICATION INFORMATION:
TELECHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-038-637-113
; Sequence 113, Application US/09038637
; Patent No. 6235470
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: La JOLLE
STATE: CA
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: KOMAL, Koichiro
APPLICANT: KOMAL, Koichiro
APPLICANT: KOMAL, Koichiro
APPLICANT: KANKEO, Hideo
ITILE OF INVENTION: DELEGONUCLEOTIDE FOR USE IN CHECKING
ITILE OF INVENTION: PRESENCE OR ABSENCE OF MOTATION IN
ITILE OF INVENTION: PRESENCE OR ABSENCE OF MOTATION IN
ITILE OF INVENTION: PRESENCE OR ABSENCE OF MOTATION IN
ITILE OF INVENTION: PRESENCE OR ABSENCE OF MOTATION IN
ITILE OF INVENTION: ASLORES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CONFORTS: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: Diskette, 5.0
OPERATING SYSTEM: IBM DOS Version 5.00
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: UP-059386/1994
FILING DATE: 29-03-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20.404000
TELEMOMENTICALION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20.404000
TELEMOMANE: SYGNESON, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20.404000
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                                                                                                                                                         Query Match 60.0%; Score 12; DB 3; Length 20; Best Local Similarity 75.0%; Pred. No. 6.1e+03; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic DNA
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MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                    1 GACCGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                   1 gacccacacaccrarrcaga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/08716459
; Patent No. 5821062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703) 205-8000
                                                    TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0182
CURRENT APPLICATION NUMBER: US/09/731,457B
CURRENT PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 30071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 315 Diskette, 1.44 Mb
MEDIUM TYPE: 315 Diskette, 1.44 Mb
MEDIUM TYPE: 315 Diskette, 1.44 Mb
MEDIUM TYPE: 1EM Compatible
OPERATING SYSTEM: 1EM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
FILOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 07/987,132
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: DECEMBER 7, 1992
ATTORNEY/AGENT INFORMATION 1.
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 2016/157
REGISTRATION NUMBER: 2016/157
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.0%; Score 11.6; DB 3; Best Local Similarity 77.8%; Pred. No. 9.9e+03; Matches 14; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 289, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Antisense Oligonucleotide US-09-731-4578-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208/157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEB: Lyon & Lyon
STREET: 633 West Pifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACCGCATAGACTTCTCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GACCACATAGATCTCTAA 19
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-291-932A-289
                                                                                                                                                                                            SEQ ID NO 14
LENGTH: 20
                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                Sequence No. 5795722
GENERAL INFORMATION:
APPLICANT: Lacroix, Jean-Michel
APPLICANT: Lacroix, Jean-Michel
APPLICANT: Lacroix, Jean-Michel
APPLICANT: Dunn, James M.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCING OF NUCLEIC ACID ANALYTES IN A SAMPLE NUMBER OF SEQUENCES:
ADDRESSES: ADDRESS:
ADDRESSES: ADDRESS:
ADSTREET: 1992 Commerce Street Suite 309
CITY: Yorktown
STATE: NY
CONTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.0%; Score 11.8; DB 2; Length 20; Best Local Similarity 86.7%; Pred. No. 7.7e+03; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10598
COMPUTER READABLE FORM:
MEDIUM TYPE Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
OFFWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGEN. P-039US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: yes
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 14, Application US/09731457B; Patent No. 6855700; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN
TELECOMMUNICATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GCATAGACTTCTCAG 19
                               CATAGACTTTTGAGA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-731-457B-14
                                                                                                                                           US-08-819-912-8
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Patent No. 6127133
GENERAL INCORMATION
Patent No. 6127133
GENERAL INCORMATION
ACCOUNTS HARDOLD, Michael A.
APPLICANT: Harpold, Michael M.
APPLICANT: Harbold, Michael M.
APPLICANT: Harbold, Michael M.
APPLICANT: Brust, Paul
TITLE OF INVENTION: RATOMATED ANALYSIS EQUIPMENT AND ASSAY METHOD FOR DETECTING CELL
TITLE OF INVENTION: PROTEIN FUNCTION USING SAME
FILE REPRENCE: 24735-515058
CURRENT APPLICATION NUMBER: US/08/229,150
CURRENT APPLICATION NUMBER: 07/812,254
EARLIER FILING DATE: 1991-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE PATENTIN VOI: 2.0
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CTHER INFORMATION: Description of Artificial Sequence:
CTHER INFORMATION: Oligonuclectide used for screening of products having
COTHER INFORMATION: EcoRI site adjacent to initiation codon of human
US-08-229-150-4
                     Gaps
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                 0;
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                 1; Indels
                 0; Mismatches
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Job time : 100 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                7 ATAGACTICICAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ATAGACTICICAG 19
                 12; Conservative
                                                                                                                                               13 ATAGAATTCTCAG 1
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                        US-08-229-150-4/c
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LENGTH: 17
                 Matches
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APPLICANT: Akong, Anthony
APPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Brust, Paul
APPLICANT: Brust, Paul
APPLICANT: Brust, Paul
APPLICANT: WINEWINON: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
TITLE OF INVENTION: METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STRATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ABM Compatible
COMPUTER: ABM COMPATER: ABM COMPATER: ABM COMPUTER: ABM COMPATER: ABM COMPATE
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                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                              Score 11.4; DB 2; Length 15;
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                           Query Match 57.0%; Score 11.4; D
Best Local Similarity 61.5%; Pred. No. 1.2e
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SISTEM: DOS

GOFWARE: FREESEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,511

CLASSIFICATION: 435

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,985

FILING DATE: 20-UNU-1994
APPLICATION NUMBER: PCT/US92/11090
FILING DATE: 18-DEC-1992
APPLICATION NUMBER: 07/812,254
FILING DATE: 20-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
RECISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9738
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-434-511-4/c
; Sequence 4, Application US/08434511
; Patent No. 6057114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.0%;
92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH. 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                             7 ATAGACTICICAG 19
                                                                                                                                                                                                                                                                                                                                                                                       |: |||::|:||
1 AUGGACUUCUCAG 13
HENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
JOPOLOGY: linear
US-08-291-932A-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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; ORIGINAL SOURCE:
US-08-434-511-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
                                                                                                                                                         June 9, 2006, 01:56:41; Search time 839 Seconds (without alignments) 292.911 Million cell updates/sec
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9412572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18892170 seqs, 6143817638 residues
                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                          1 gaccgcatagacttctcaga 20
                                                                                                                                                                                                                                                                                                                                                                                            IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                  US-09-743-825-10
20
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65:
77:
10:
11:
13:
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Perfect score:
Sequence:
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                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			•			SUMMARIES	
Reg	Result		Query				
i	S.	Score	Match	Match Length DB	图	ID	Description
	Н	14	70.0	19	14	US-11-083-784-577386	Sequence 577386,
	~	14	70.0	19	15	US-11-101-244-577386	
υ	m	13.8	69.0	19	14	US-11-083-784-818386	
	4	13.8	69.0	19	14	US-11-083-784-1312885	
υ	ī	13.8	69.0	19	15	US-11-101-244-818386	
	9	13.8	69.0	19	15	US-11-101-244-1312885	Sequence 1312885,
	7	13.8	69.0	20	7	US-10-289-762-2812	Sequence 2812, Ap
	æ	13.4	67.0	19	14	US-11-083-784-189820	Sequence 189820,
	σ	13.4	67.0	19	14	US-11-083-784-189920	Sequence 189920,
U	10	13.4	67.0	19	14	US-11-083-784-511937	
	11	13.4	67.0	19	14	US-11-083-784-1082194	Sequence 1082194,
	12	13.4	67.0	19	15	US-11-101-244-189820	Sequence 189820,
	13	13.4	67.0	19	15	US-11-101-244-189920	Sequence 189920,
U	14	13.4	67.0	19	15	US-11-101-244-511937	Sequence 511937,
	12	13.4	67.0	19	15	US-11-101-244-1082194	Sequence 1082194,
	16	13.2	0.99	19	14	US-11-083-784-1065181	Sequence 1065181,
	11	13.2	0.99	19	14	US-11-083-784-1500214	Sequence 1500214,

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Gaps

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70.0%; Score 14; DB 14; Length 19; 78.6%; Pred. No. 3.6e+03; tive 3; Mismatches 0; Indels

1 GACCGCATAGACTT 14 GACCGCAUAGACUU 19

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RESULT 2 US-11-101-244-577386

Best Local Similarity 78.6 Matches 11; Conservative

Query Match

Sequence 1065181, Sequence 48, Appl Sequence 6652, A Sequence 66629, A Sequence 66629, A Sequence 66629, A Sequence 66629, A Sequence 66629, A Sequence 66728, A Sequence 66728, A Sequence 6728, A Sequence 131661, Sequence 13261, A Sequence 132624, Sequence 1324218, Sequence 1267211, A Sequence 1267211, A Sequence 928551,	
	ALIGNMENTS 11083784 and Hyperfunctional siRNA 11/083,784 8 8/714,333 12,050 16,137
19 15 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	11cation US/1050245475A1  n, Inc. a, Anastasia ls, Angela Devin 1, William le, Stephen 99US 1 NUMBER: US/10/2003-11-14 2003-10-14 2003-11-14 S: 1591911 ry
00000000000000000000000000000000000000	pplic 20050 (n), (n), (va, 11ds, 1ds,
	01 102 - 102 - 103 - 10
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US-11-083-784-1312885
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           Sequence 5/186, Application US/11101244

Fublication No. US205050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
FRIOR RPLICATION NUMBER: 60/502,050
PRIOR PELING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 577386
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14; DB 15; Length 19
Pred. No. 3.6e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 818386, Application US/11083784
Publication No. US20050245475A1
GENERAL INPORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Kryorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SEQ ID NO 818386
LENGTHR: 19
Sequence 577386, Application US/11101244
Publication No. US20050246794A1
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Best Local Similarity 78.6%;
Matches 11; Conservative
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Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-577386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-083-784-818386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-083-784-818386/c
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RESULT 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0%; Score 13.8; DB 14; Length 19; 70.6%; Pred. No. 4.6e+03; Live 3; Mismatches 2; Indels
                                                           GENERAL INCOMPATION;
GENERAL INCOMPATION;
APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Asrablal, William
APPLICANT: Asrablal, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
FRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF ESQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1312885
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Khorova, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR PAPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-10
PRIOR PLILING DATE: 2003-10
PRIOR PLILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PRODECTORY
SEQ ID NO 918386
Sequence 1312885, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 818386, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CGCATAGACTTCTCAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCAAAGCCUUCUCAGA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-101-244-818386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 189920, Application US/11083784
; Sequence 189920, Application US/11083784
; Sequence 189920, Application No. USZO050245475A1
; GENERAL INFORMATION:
; APPLICANT: Caring Anstasia
; APPLICANT: Reynolds, Anstasia
; APPLICANT: Reynolds, Anstasia
; APPLICANT: Reynolds, Anstasia
; APPLICANT: Beake Devin
; APPLICANT: Beake Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; PILE REFERENCE: 1349918
; CURRENT APPLICATION: NUMBER: US/11/083,784
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-11-14
; SUPPLICATION NUMBER: GO/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTHARE: PROPLICATY
; SEQ ID NO 189920
                                                              APPLICANT: Scatinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
TITLE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
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US-11-083-784-511937/c
; Sequence 511937, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S GCATAGACTTCTCAG 19
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Best Local Similarity 73.3
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-189820
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US-11-083-784-189920
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection
FILE REPREMENTE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT PILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
LENGTH: 20
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RESULT 6
US-11-101-244-1312885
US-11-101-244-1312885
Sequence 1312865, Application US/11101244
Fublication No. US20050246794A1
GENERAL INCOMMATION:
APPLICANT: Diarmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Ansthall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2002-010
PRIOR FILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1312885
LENGTH: 11
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Best Local Similarity 70.6%; Pred. No. 4.6e+03;
Matches 12; Conservative 3; Mismatches
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Kivorova, Anastasia
APPLICANT: Reyolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2812, Application US/10289762
Publication No. US20040006218A1
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACCGCATAGACTTCTC 17
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; ORGANISM: Homo sapiens
US-11-101-244-1312885
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Publication No. US20050246794A1
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CORGANISM: Homo sapiens
US-11-101-244-189820
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Best Local Similarity
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Pred. No. 7.6e+03;
4; Mismatches 1; Indels
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Argenal
APPLICANT: Argenal
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PELING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PELING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1082194, Application US/11083784

Sequence 1082194, Application US/11083784

Rublication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Characon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Respect Set Sephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT FILING DATE: 2005-03-18

PRIOR FILING DATE: 2003-11.14

PRIOR PLILOATION NUMBER: 60/426,137

PRIOR PLILOATION NUMBER: 60/426,137

PRIOR PLILOATION NUMBER: 60/426,137

PRIOR PLILOATION NUMBER: 60/426,137

PRIOR PLILNG DATE: 2002-11.14

SEQ ID NOS: 1591911

SEQ ID NO 1082194
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US-11-101-244-189820
; Sequence 189820, Application US/11101244
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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CAUCGACUUCUCAGA 15
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Best Local Similarity 66.7"
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CORGANISM: Homo sapiens
US-11-083-784-511937
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CORGANISM: Homo sapiens
US-11-083-784-1082194
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GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scarings, Stephen
APPLICANT: Scarings, Stephen
TILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 189820
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APPLICANT: Krynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 189920
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Pred. No. 7.6e+03;
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1.1 Similarity 73.3%; Pred. No. 7.6e+03;
11; Conservative 3; Mismatches 1;
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Sequence 189920, Application US/11101244
Publication No. US20050246/94A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-11-101-244-511937/c
Sequence 511937, Application US/11101244
Publication No. US20050246794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.0%;
Best Local Similarity 73.3%;
Matches 11; Conservative
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GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Respect bevin
APPLICANT: Beake, Devin
APPLICANT: Bearinge, Stephen
TILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
SOFTWARR: POPTICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2002-11-14
SOFTWARR: POPTICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2002-11-14
SOFTWARR: POPTICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2002-11-14
SOFTWARR: POPTICATION STEPPICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2003-11-14
SOFTWARR: PROPTICATION STEPPICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2003-11-14
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| Publication No. US20050246794A1
| GENERAL INPORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Stephen
| APPLICANT: Acaringe, Stephen
| TILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: US/11/101,244
| CURRENT PELLOATION NUMBER: 60/502,050
| PRIOR APPLICATION NUMBER: 60/502,050
| PRIOR PLILING DATE: 2003-09-10
| PRIOR PLILING DATE: 2003-01-14
| NUMBER OF SEQ ID NOS: 1591911
| SOFTWARE: PROPRIETARY
| SEQ ID NO 1082194
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Best Local Similarity 66.74
Matches 10; Conservative
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CORGANISM: Homo sapiens
US-11-101-244-511937
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; ORGANISM: Homo sapiens
US-11-101-244-1082194
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US-11-101-244-1082194
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Search completed: June 9, 2006, 02:12:17 Job time : 840 secs Colosu) Midle acot sin,

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RESULT 2
US-10-514-776-214/c
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SEQ ID NO 45
LENGTH: 20
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201, App
18, Appl
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                                                 June 9, 2006, 01:58:21; Search time 23 Seconds (without alignments) 110.368 Million cell updates/sec
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                                                                                                                                                                                                                         Published Applications NA New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-514-45-214
US-11-251-465-365
US-11-251-465-38
US-11-293-697-5435
US-11-293-697-5435
US-11-293-697-5435
US-11-251-465-371
US-10-469-938A-158
US-10-469-938A-158
US-11-251-465-201
US-10-469-938A-158
US-11-251-465-201
US-11-251-465-201
US-11-251-465-201
US-11-251-465-201
US-11-251-465-201
US-11-261-473-358
US-11-261-761-268
US-11-265-761-268
US-11-265-761-268
US-11-261-761-268
                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-324-230-4
US-11-110-361A-84
                                                                                                                                       253354 seqs, 63461778 residues
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Maximum Match 100%
Listing first 45 summaries
                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
                                                                                                                Scoring table:
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442, App
441, App
847, App
5255, Ap
167, App
1177, App
115, App
116, App
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10, Appl
10, Appl
32, Appl
25, Appl
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: Primer
OTHER 118-279-45
                                                                                                                                                                                                           Sequence
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Pred. No. 4.1e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45. Application US/11189279
Sequence 45. Application US/11189279
Publication No. US20060115829A1
GENERAL INFORMATION:
APPLICANT: MAO, LI
APPLICANT: WANG, JIE
APPLICANT: LUO, WANG
TILLE OF INVENTION: A METHOD OF TREATING CANCER;
FILE REFERENCE: UTXC:875US
CURRENT FILING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: 05/11/189,279
CURRENT FILING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 69
US-11-293-697-5287

US-10-511-937-2016

US-10-514-776-28

US-10-513-83-76

US-11-123-692-10

US-11-125-980-10

US-11-255-980-10

US-11-255-980-10

US-11-293-697-5317

US-11-293-697-5317

US-11-293-697-5255

US-11-251-465-847

US-11-293-697-5255

US-11-293-697-5255

US-11-293-697-5255

US-11-293-697-5255

US-10-514-776-199

US-10-514-776-199

US-10-515-817-115
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TITLE OF INVENTION: CK primer
FILE REFERENCE: GP03-1006PCT
CURRENT APPLICATION NUMBER: US/10/514,776
CURRENT FILING DATE: 2004-11-19
PRIOR APPLICATION NUMBER: JP P2002-145689
PRIOR PLILOR DATE: 2002-05-21
PRIOR APPLICATION NUMBER: JP P2002-175271
PRIOR PILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 214, Application US/10514776; Publication No. US20060094008A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACCGCATAGACTTCTCAGA 20
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Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/AU01/00729
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.2
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CRGANISM: Homo mapiens
US-10-511-937-993
                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-264-558-38
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                                                                                                                   SEQ ID NO 38
LENGIH: 20
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Sequence 365, Application US/11251465

Publicantion No. US20060094061A1

Sequence 365, Application US/11251465

Publicant No. US20060094061A1

APPLICANT: Brys, Reginald

APPLICANT: Vandeghinate, Nick

APPLICANT: Tomme, Peter

TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The

TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION: Inflammatory Diseases

TITLE OF INVENTION WUMBER: US/11/251,465

CURRENT PELLING DATE: 2005-10-14

PRIOR PELLING DATE: 2004-10-15

NUMBER OF SEQ ID NOS: 890

SOFTWARE: Patentin Version 3.3

LENGTH: 19
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Publication No. US20060088913A1
GENERAL INFORMATION:
APPLICANT: Blonomics Limited
APPLICANT: Mullace, Robyn H
APPLICANT: Mullace, Robyn H
APPLICANT: Mullace, Samuel F
APPLICANT: Mullace, Samuel F
APPLICANT: Dibbens, Leanne M
TITLE OF INVENTION: MUTATION ASSOCIATED WITH EPILEPSY
FILE REFERENCE: 1386/10/2
CURRENT FILING DATE: 2005-11-01
PRIOR APPLICATION NUMBER: US/11/264,558
                                                                                                                                                                                                         ; OTHER INFORMATION: Designed DNA based on CK18
US-10-514-776-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Knock-down target sequence US-11-251-465-365
PRIOR APPLICATION NUMBER: JP P2002-199759
PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 474
SSOTWARE: PatentIn version 3.1
SSO ID NO 214
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                       2 ACCGCATAGACTTCTCAG 19
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                                                                                                                                                            ORGANISM: Artificial
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US-11-264-558-38/c
                                                                                                                                           TYPE: DNA
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APPLICANT: Mohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Worris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT APPLICATION NUMBER: US/10/131,831
PRIOR PELING DATE: 2002-04-24
PRIOR PELING DATE: 2002-04-24
PRIOR PELING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Query Match 50.0%; Score 10; DB 7; Length 20; Best Local Similarity 100.0%; Pred. No. 4.8e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 5435, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILLE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILLING DATE: 2005-12-05
PRIOR FILLING DATE: 2005-12-05
PRIOR FILLING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: EXPRESSION DIAGNOSTICS, INC.
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Publication No. US20060088836A1
GENERAL INFORMATION:
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Gaps
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Sequence 158, Application US/10469938A

Publication vo. US20660105329A1

GENERAL INFORMATION:
TITLE OF INVENTION: Gene Panel
TITLE OF INVENTION: Gene Panel
CURRENT APPLICATION NUMBER: US/10/469,938A

CURRENT PPLICATION NUMBER: US/2001-070940

PRIOR FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 192

SOFTWARE: Patentin Ver. 2.0
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| Sequence 704, Application US/10511937
| Publication No. US2006008836A1
| GENERAL INFORMATION:
| APPLICANT: EXPRESSION DIAGNOSTICS, INC.
| APPLICANT: Wohlgemuth, Jay
| APPLICANT: Prentice, James
| APPLICANT: MacDonald
| APPLICANT: MacDonald
| APPLICANT: MACDONALD
| APPLICANT: MACDONALD
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
| TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
| FILE REFERENCE: 50661200104
| CURRENT APPLICATION NUMBER: US 10/511,937
| CURRENT PELLING DATE: 2004-10-19
| PRIOR PILING DATE: 2003-04-24
| PRIOR PLILING DATE: 2002-04-24
| PRIOR APPLICATION NUMBER: US 10/131,831
| PRIOR FILING DATE: 2002-04-24
| PRIOR APPLICATION NUMBER: US 10/325,899
| PRIOR FILING DATE: 2002-12-20
| NUMBER OF SEQ ID NOS: 3117
| SOFTWARE: PATENTIN VUMBER: US 10/325,899
| SEQ ID NO 704
                                                                                                                                                                                                                                                    Query Match

46.0%; Score 9.2; DB 7; Length 19;
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels
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Pred. No. 1.3e+04;
                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Knock-down target sequence
US-11-251-465-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
           SOFTWARE: PatentIn version 3.3
                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 78.6%;
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ORGANISM: Homo sapiens
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                                    SEQ ID NO 371
LENGTH: 19
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Publication No. US20060094061A1
SEQUENCE 371, Application No. US20060094061A1
SEQUENCE INPORTATION:
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter:
APPLICANT: Tomme, Peter:
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Same, USeful In The Treatment Of Joint Degenerative And
TITLE OF INVENTION: UNMERR: US/11/251,465
CURRENT APPLICATION NUMBER: US/11/251,465
FRICK FILING DATE: 2005-10-14
FRICK FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
                                                                                                                                                          FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized

US-11-293-697-5435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/11247332
Publication No. US20060094667A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Glucopyranosyloxypyrazole Derivatives and Use Thereof in
TITLE OF INVENTION: Medicines
TITLE OF INVENTION: Medicines
TITLE OF INVENTION: Medicines
TITLE REFERENCE: Q76132
CURRENT APPLICATION NUMBER: US/11/247,332
CURRENT APPLICATION NUMBER: US/10/451,926
PRIOR PILING DATE: 2003-06-27
PRIOR PILING DATE: 2003-06-27
PRIOR FILING DATE: 2001-12-25
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 20
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48.0%; Score 9.6; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 12; Conservative 0; Mismatches 4; Indels
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48.0%; Score 9.6; DB 7; Length 20;
Best Local Similarity 75.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 4; Indels
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                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5435
LENGTH: 18
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US-11-251-465-371/c
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US-11-251-465-201
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vo-11-221-40-201, Application US/11251465
publication No. US20060094061A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandesphinste, Nick
APPLICANT: Tomme, Peter
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: Inflammatory Diseases
TITLE OF INVENTION: 101/2-A USA
CURRENT APPLICATION NUMBER: US/11/251,465
CURRENT PILING DATE: 2005-10-14
PRIOR PILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: Patentin version 3.3
SEQ ID NO 201
LENGTH: 19
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US-10-469-938A-63
i Sequence 6.3, Application US/10469938A
j Publication No. US20060105329A1
j GENERAL INFORMATION:
j APPLICANT: Ajinomoto Co., Inc.
j TITLE OF INVENTION: Gene Panel for Genes Involving Liver Regeneration
f FILE REFERENCE: B866AYOF133
j CURRENT APPLICATION NUMBER: US/10/469,938A
j CURRENT AILING DATE: 2003-09-05
j PRIOR FILING DATE: 2001-03-13
j NUMBER OF SEQ ID NOS: 192
j SOFFWARE: Patentin Ver. 2.0
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                                       TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: primer
US-10-469-938A-158
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                                                                                                                                                                                        Length 20;
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46.0%; Score 9.2; DB 6; Length 20
Best Local Similarity 78.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                          2 ACCGCATAGACTTC 15
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SEQ ID NO 158
LENGTH: 20
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LENGTH: 18
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; OTHER INFORMATION: Description of Artificial Sequence: sense upstream vector Primer; OTHER INFORMATION: ADJ014
US-10-521-008-6
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Publication No. US20060099175A1
GENERAL INFORMATION:
APPLICANT: Van Den Hazel, Bart
APPLICANT: Van Den Hazel, Bart
APPLICANT: Andersen, Kim V.
TITLE OF INVENTION: Phill-length Interferon Gamma Polypeptide Variants
FILE REFERENCE: 16384US04
CURRENT APPLICATION NUMBER: US/10/521,008
CURRENT PILING DATE: 2005-01-03
FRIOR APPLICATION NUMBER: PCT/DK03/000426
PRIOR PILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6

LENGTH: 19
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APPLICANT: Ommen van, Garrit-Jan B.
APPLICANT: Deutekom van, Judith C.T.
APPLICANT: Deutekom van, Judith C.T.
APPLICANT: Deutekom van, John C.T.
APPLICANT: Deutekom van, John C.T.
APPLICANT: Aartema-Rus, Annemieke T.
TITLE OF INVENTION: interfering with the secondary RNA structure FILE REPRENCE: P639170500
CURRENT APPLICATION NUMBER: US/11/233,507
CURRENT FILING DATE: 2005-09-21
PRIOR PILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: PCT/NL2004/00196
PRIOR PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 18
LENGTH: 18
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US-11-233-507-18
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                         45.0%; Score 9; DB 7; Length 19; 100.0%; Pred. No. 1.6e+04;
                                      100.0%; Pred. ...
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; Sequence 18, Application US/11233507
; Publication No. US2006009616A1
; GENERAL INFORMATION:
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                                                                           Conservative
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Query Match
Best Local Similarity
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Query Match

44.0%; Score 8.8; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                         RESULT 15
US-10-524-399-14
Sequence 14, Application US/10524399
Sequence 14, Application US/10524399
PUDLICATION NO. US20060099591A1
GENERAL INFORMATION:
APPLICANT: KRAUER, Addreas
APPLICANT: RAULF, Friedrich
APPLICANT: SCHERER, Addreas
ITLE OF INVENTION Diagnosis of chronic rejection
FILE REFERENCE: 4-32608A
CURRENT APPLICATION NUMBER: US/10/524,399
CURRENT FILING DATE: 2005-02-11
FRIOR RILING DATE: 2005-02-11
FRIOR RILING DATE: 2005-02-11
FRIOR FILING DATE: 2005-02-11
FRIOR FILING DATE: 2005-03-11
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19 ATAGACCTCCCA 8
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Search completed: June 9, 2006, 02:12:47 Job time : 24 Becs

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